

Result No.	Score	Query	Match	Length	DB ID	Description
1	31	1.5	31	22	AA130734	Human silent noncoding gene AAH41500 PCR primer used to Human gene single nucleotide polymorphism (SNP) HCK 1.
2	31	1.5	31	22	AA130735	Human gene single nucleotide polymorphism (SNP) HCK 1.
3	31	1.5	31	22	AA130736	Human gene single nucleotide polymorphism (SNP) HCK 1.
4	31	1.5	31	22	AA130737	Human gene single nucleotide polymorphism (SNP) HCK 1.
5	31	1.5	31	22	AA130738	Human gene single nucleotide polymorphism (SNP) HCK 1.
c 6	27	1.3	33	22	AAH1498	Human tyrosine kinase receptor m
c 7	26	1.3	32	22	AAH1491	Human tyrosine kinase receptor m
c 8	26	1.3	32	22	AAH1492	Human tyrosine kinase receptor m
c 9	25	1.2	32	22	AAH41501	Human tyrosine kinase receptor m

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

RESULT	1	ID	AA130734	standard; DNA; 31 BP.
		XX	AA130734;	
		AC		
		XX		18-OCT-2001 (first entry)
		DT		Human single nucleotide polymorphism (SNP) HCK 1.

## ALIGNMENTS



XX Cargill M, Ireland JS, Lander ES;  
 XX WPI; 2001-522952/57.  
 XX Nucleic acid molecules from the human genome which include polymorphic sites, useful in methods for predicting the presence, absence or severity of a particular phenotype or disorder (e.g. diabetes)  
 PT associated with a particular genotype -  
 XX  
 PS Claim 1; Page 104; 145pp; English.  
 XX  
 CC The invention relates to the identification of nucleic acid molecules (AAI29513-AAI31314) from the human genome which include polymorphic sites which can predispose individuals to disease. Various genes from a number of individuals were resequenced and single nucleotide polymorphisms (SNPs) in these genes discovered. The method is useful for predicting the presence, absence or severity of a particular phenotype or disorder (e.g. diabetes) associated with a particular genotype. The nucleic acids containing the polymorphic sites may be useful in forensics and paternity testing.

XX Sequence 31 BP; 7 A; 7 C; 10 G; 7 T; 0 other;  
 SQ Query Match Score 1.5%; Best Local Similarity 100.0%; Pred. No. 7.6e-05; Length 31;  
 CC  
 CC (AAI29513-AAI31314) from the human genome which include polymorphic sites which can predispose individuals to disease. Various genes from a number of individuals were resequenced and single nucleotide polymorphisms (SNPs) in these genes discovered. The method is useful for predicting the presence, absence or severity of a particular phenotype or disorder (e.g. diabetes) associated with a particular genotype. The nucleic acids containing the polymorphic sites may be useful in forensics and paternity testing.

XX Sequence 31 BP; 6 A; 9 C; 6 G; 10 T; 0 other;

RESULT 4  
 AAI30737  
 ID AAI30737 standard; DNA; 31 BP.  
 XX  
 AC AAI30737;  
 XX DT 18-OCT-2001 (first entry)  
 DE Human single nucleotide polymorphism (SNP) HCK 4.  
 KW Human; resequence; genotype; disease; forensic; paternity testing;  
 KW single nucleotide polymorphism; SNP; ss.  
 OS Homo sapiens.  
 XX FH Human single nucleotide polymorphism (SNP) HCK 4.  
 XX DE Human single nucleotide polymorphism (SNP) HCK 4.  
 KW Human; resequence; genotype; disease; forensic; paternity testing;  
 KW single nucleotide polymorphism; SNP; ss.  
 OS Homo sapiens.  
 XX Key Location/Qualifiers  
 XX Variation replace(16,G)  
 FT /\*tag= a  
 FT /standard\_name= "single nucleotide polymorphism"  
 XX PA WO200166800-A2.  
 PN WO200166800-A2.  
 XX  
 PD 13-SEP-2001.  
 XX DR 07-MAR-2001; 2001WO-US07268.  
 XX PR 07-MAR-2001; 2001WO-US07268.  
 PR 07-MAR-2000; 2000US-0187510.  
 PR 22-MAY-2000; 2000US-0206129.  
 XX PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
 XX  
 PI Cargill M, Ireland JS, Lander ES;  
 XX DR 07-MAR-2001; 2001WO-US07268.  
 XX PR 07-MAR-2000; 2000US-0187510.  
 PR 22-MAY-2000; 2000US-0206129.  
 XX PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
 XX  
 PI Cargill M, Ireland JS, Lander ES;  
 XX DR 2001-522952/57.  
 XX Nucleic acid molecules from the human genome which include polymorphic sites, useful in methods for predicting the presence, absence or severity of a particular phenotype or disorder (e.g. diabetes) associated with a particular genotype -  
 XX  
 CC The invention relates to the identification of nucleic acid molecules (AAI29513-AAI31314) from the human genome which include polymorphic sites which can predispose individuals to disease. Various genes from a number of individuals were resequenced and single nucleotide polymorphisms (SNPs) in these genes discovered. The method is useful for predicting the presence, absence or severity of a particular phenotype or disorder (e.g. diabetes) associated with a particular genotype.

CC diabetes) associated with a particular genotype. The nucleic acids  
CC containing the polymorphic sites may be useful in forensics and paternity  
CC testing.

SQ Sequence 31 BP; 12 A; 11 C; 5 G; 3 T; 0 other;

Query Match 6  
Best Local Similarity 100.0%; Score 31; DB 22; Length 31;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 219 aaaaactgaaaccaggccacgtt 249  
DB 1 aaaaactgaaaccaggccacgtt 31

RESULT 6  
AAH41498/C  
ID AAH41498 standard; DNA; 33 BP.  
XX  
AC AAH41498;  
XX DT 23-AUG-2001 (first entry)  
XX DE Human tyrosine kinase Hck PCR primer SEQ ID NO:10.  
XX KW Human; tyrosine kinase Hck binding protein; tyrosine kinase; Hck;  
KW tumour lethal factor; tumour necrosis factor alpha; apoptosis; HSB-1;  
KW Hck signal transduction; human immunodeficiency virus; HIV infection;  
KW anticancer; PCR primer; ss.  
OS Homo sapiens.  
XX PN WO200132869-A1.  
XX PD 10-MAY-2001.  
XX PT 26-OCT-2000; 2000WO-JP07500.  
XX PR 29-OCT-1999; 99JP-0309957.  
XX PA (SSSE ) SSP CO LTD.  
XX PI Taniyama T, Narita T;  
XX PN WO200132869-A1.  
XX PD 10-MAY-2001.  
XX PT 26-OCT-2000; 2000WO-JP07500.  
XX PR 29-OCT-1999; 99JP-0309957.  
XX PA (SSSE ) SSP CO LTD.  
XX PI Taniyama T, Narita T;  
XX DR 2001-316440/33.  
XX PT New proteins which bind to human tyrosine kinase Hck for promotion of  
PT apoptosis and for the elucidation of the mechanism of Hck signal  
PT transduction.  
XX PS Example 1; Page 30; 45pp; Japanese.

The present invention describes a protein, designated HSB-1, which binds  
CC to human tyrosine kinase Hck. Also described are: (1) nucleic acids  
CC containing the protein and its derivatives; (2) recombinant vectors  
CC vectors and expressing the protein. HSB-1 has cytostatic activity, binds  
CC tyrosine kinase, enhances tumour necrosis factor alpha and promotes  
CC apoptosis. HSB-1 proteins are used for the elucidation of the mechanism  
CC of Hck signal transduction and of the role of Hck in human  
CC immunodeficiency virus (HIV) infection. They can be used for the  
CC treatment of infections and other diseases with which Hck is associated.  
CC They promote the anticancer activity of tumour necrosis factor alpha.  
CC The present sequence represents a PCR primer used in the cloning of  
CC HSB-1, which is used in an example from the present invention.  
XX SQ Sequence 33 BP; 8 A; 5 C; 9 G; 10 T; 0 other;  
XX PS Example 3; Page 33; 45pp; Japanese.  
CC The present invention describes a protein, designated HSB-1, which binds  
CC to human tyrosine kinase Hck. Also described are: (1) nucleic acids  
CC encoding the protein and its derivatives; (2) recombinant vectors  
CC containing the nucleic acids; and (3) host cells transformed by the  
CC vectors and expressing the protein. HSB-1 has cytostatic activity, binds  
CC tyrosine kinase, enhances tumour necrosis factor alpha and promotes  
CC apoptosis. HSB-1 proteins are used for the elucidation of the mechanism  
CC of Hck signal transduction and of the role of Hck in human  
CC immunodeficiency virus (HIV) infection. They can be used for the  
CC treatment of infections and other diseases with which Hck is associated.  
CC They promote the anticancer activity of tumour necrosis factor alpha.  
CC The present sequence represents a PCR primer for the human tyrosine  
CC kinase Hck, which is used in an example from the present invention.  
XX SQ Sequence 33 BP; 2 A; 8 C; 11 G; 12 T; 0 other;

Query Match 1.3%; Score 27; DB 22; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.0071; Mismatches 0; Indels 0; Gaps 0;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8  
AAH41492/C  
ID AAH41492 standard; DNA; 32 BP.  
XX

CC diabetes) associated with a particular genotype. The nucleic acids  
CC containing the polymorphic sites may be useful in forensics and paternity  
CC testing.

SQ Sequence 31 BP; 12 A; 11 C; 5 G; 3 T; 0 other;

Query Match 7  
Best Local Similarity 100.0%; Score 31; DB 22; Length 31;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1657 acagagccgttaccaacagcggcca 1683  
DB 33 ACAGAGCCAGTACGACAGGCCA 7

RESULT 7  
AAH41491  
ID AAH41491 standard; DNA; 32 BP.  
XX  
AC AAH41491;  
XX DT 23-AUG-2001 (first entry)  
XX DE Human tyrosine kinase Hck binding protein cloning PCR primer SEQ ID NO:3.  
XX KW Human; tyrosine kinase Hck binding protein; tyrosine kinase; Hck;  
KW tumour lethal factor; tumour necrosis factor alpha; apoptosis; HSB-1;  
KW Hck signal transduction; human immunodeficiency virus; HIV infection;  
KW anticancer; PCR primer; ss.  
XX OS Homo sapiens.  
XX PN WO200132869-A1.  
XX PD 10-MAY-2001.  
XX PT 26-OCT-2000; 2000WO-JP07500.  
XX PR 29-OCT-1999; 99JP-0309957.  
XX PA (SSSE ) SSP CO LTD.  
XX PI Taniyama T, Narita T;  
XX PN WO200132869-A1.  
XX PD 10-MAY-2001.  
XX PT 26-OCT-2000; 2000WO-JP07500.  
XX PR 29-OCT-1999; 99JP-0309957.  
XX PA (SSSE ) SSP CO LTD.  
XX PI Taniyama T, Narita T;  
XX DR 2001-316440/33.  
XX PT New proteins which bind to human tyrosine kinase Hck for promotion of  
PT apoptosis and for the elucidation of the mechanism of Hck signal  
PT transduction.  
XX PS Example 1; Page 30; 45pp; Japanese.

The present invention describes a protein, designated HSB-1, which binds  
CC to human tyrosine kinase Hck. Also described are: (1) nucleic acids  
CC containing the protein and its derivatives; (2) recombinant vectors  
CC vectors and expressing the protein. HSB-1 has cytostatic activity, binds  
CC tyrosine kinase, enhances tumour necrosis factor alpha and promotes  
CC apoptosis. HSB-1 proteins are used for the elucidation of the mechanism  
CC of Hck signal transduction and of the role of Hck in human  
CC immunodeficiency virus (HIV) infection. They can be used for the  
CC treatment of infections and other diseases with which Hck is associated.  
CC They promote the anticancer activity of tumour necrosis factor alpha.  
CC The present sequence represents a PCR primer used in the cloning of  
CC HSB-1, which is used in an example from the present invention.  
XX SQ Sequence 32 BP; 8 A; 5 C; 9 G; 10 T; 0 other;

Query Match 1.3%; Score 26; DB 22; Length 32;  
Best Local Similarity 100.0%; Pred. No. 0.022; Mismatches 0; Indels 0; Gaps 0;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 350 tcgtggatgcctgtatcattacgag 375  
DB 7 tcgtggatgcctgtatcattacgag 32

RESULT 8  
AAH41492/C  
ID AAH41492 standard; DNA; 32 BP.  
XX



XX (CURA-) CURAGEN CORP.  
 PA PT New proteins which bind to human tyrosine kinase Hck for promotion of  
 XX PT apoptosis and for the elucidation of the mechanism of Hck signal  
 PI PT transduction -  
 XX  
 DR WPI; 2001-355949/37.

XX Isolated human nucleic acids comprising one or more single nucleotide polymorphisms useful for treating a subject suffering from a pathology, e.g. autoimmune diseases, ascribed to the presence of a sequence polymorphism -

XX Claim 1; Page 359; 674pp; English.

XX ABL0010 to ABL0104 represent human nucleic acid oligonucleotides comprising one or more single nucleotide polymorphisms (SNPs). ABB56531  
 CC to ABB5693 represent human peptides encoded by some of the SNP  
 CC oligonucleotides. The sequences from the present invention can have immunosuppressive, cytostatic, antinflammatory, neuroprotective and antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides and antibodies from the present invention can be used for treating a subject suffering from, at risk for, or suspected of, suffering from a pathology ascribed to the presence of a sequence polymorphism. The pathology may be autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. The SNPs are also useful for determining which forms of a characterised polymorphism are present in individuals. The antibodies may be used in the detection, quantitation and/or cellular or tissue localisation of a polymorphic protein (e.g., for use in measuring levels of the polymorphic protein within appropriate physiological samples).

XX Sequence 51 BP; 10 A; 17 C; 13 G; 11 T; 0 other;

XX Query Match 1.28; Score 25; DB 23; Length 51;  
 Best Local Similarity 100.0%; Pred No. 0.068; Indels 0; Gaps 0;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX The present invention describes a protein, designated HSB-1, which binds to human tyrosine kinase Hck. Also described are: (1) nucleic acids encoding the protein and its derivatives; (2) recombinant vectors containing the nucleic acids; and (3) host cells transformed by the vectors and expressing the protein. HSB-1 has cytostatic activity, binds tyrosine kinase, enhances tumour necrosis factor alpha and promotes apoptosis. HSB-1 proteins are used for the elucidation of the mechanism of Hck signal transduction and of the role of Hck in human immunodeficiency virus (HIV) infection. They can be used for the treatment of infections and other diseases with which Hck is associated. They promote the anticancer activity of tumour necrosis factor alpha. The present sequence represents a PCR primer used in the cloning of HSB-1, which is used in an example from the present invention.

XX SQ Sequence 32 BP; 9 A; 4 C; 10 G; 9 T; 0 other;

XX Query Match 1.28; Score 24; DB 22; Length 32;  
 Best Local Similarity 100.0%; Pred No. 0.21; Indels 0; Gaps 0;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Qy 529 gagggatggtttcaaggccat 552  
 YY 9 gaggatggtttcaaggccat 32  
 Db 9 gagggatggtttcaaggccat 32

XX RESULT 12  
 AAC90044  
 ID AAC90044 standard; DNA; 78 BP.  
 XX AAC90044;  
 AC AAC90044;  
 XX DT 13-MAR-2001 (first entry)  
 DE PCR Primer used to create a library of RRT-Hck SH3 domains.  
 XX KW SH3 domain; human; Src homology region 3 domain; RT-loop; Hck protein;  
 KW PCR primer; ss.  
 XX OS Homo sapiens.  
 XX PN WO200072742-A2.  
 XX PD 07-DEC-2000.  
 XX PF 26-MAY-2000; 2000WO-FI00477.  
 XX PR 26-MAY-1999; 99US-0136085.  
 XX PA (SAKSEA K.  
 XX PI Sakseila K, H.Iipakka M.  
 XX DR WPI; 2001-061424/07.

XX WO200132869-A1.

XX PD 10-MAY-2001.  
 XX PP 26-OCT-2000; 2000WO-FP07500.  
 XX PR 29-OCT-1999; 99JP-030957.  
 XX PA (SSSE ) SSP CO LTD.  
 XX PI Tanigawa T, Narita T;  
 XX DR WPI; 2001-316440/33.

XX A method for generating Src homology region 3 (SH3) domains with tailored binding properties or artificial SH3 domains, comprises employing random manipulation of the SH3 RT-loop sequence -  
 XX PS Example 1; Page 10; 34pp; English.

XX The present invention relates to a method for generating Src homology region 3 (SH3) domains with tailored binding properties or artificial SH3 domains, comprises producing a collection of SH3 domains containing a randomised RT-loop (RRT-SH3 domains). Human p59 Hck was used in the present invention as the SH3 domain. The present sequence is a PCR primer, which

CC was used to create a library of RRT-HCK SH3 domains. The generated SH3 domains are useful for inhibiting, activating or modifying the functions of cellular or pathogen-encoded proteins for research or therapeutic purposes.

XX Sequence 78 BP; 13 A; 13 C; 17 G; 17 T; 18 other;

Query Match 1.2%; Score 24; DB 22; Length 78;  
Best Local Similarity 100.0%; Pred. No. 0.21;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 391 gacctcgttccagaaggggac 414  
||||| ||||| ||||| |||||  
Db 55 gacctcgttccagaaggggac 78

RESULT 13  
AAF95624  
ID AAF95624 standard; DNA; 21 BP.  
XX  
AC AAF95624;  
XX DT 06-JUN-2001 (first entry)

XX Human gene single nucleotide polymorphism #385.  
DE Human; variant thrombospondin 1; variant thrombospondin 4; SNP;  
KW polymorphism; vascular disease; coronary artery disease; forensics;  
KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;  
KW pulmonary embolism; paternity test; ds.  
XX Homo sapiens.  
OS Homo sapiens.  
XX FH Key Variation  
FT Location/Qualifiers  
FT replace(11,C)  
FT /\*tag= a  
FT /standard\_name= "single nucleotide polymorphism"  
XX PN WO200118250-A2.  
XX PD 15-MAR-2001.

XX PN WO200118250-A2.  
XX PD 15-MAR-2001.  
XX PF 07-SEP-2000; 2000WO-US24503.  
XX PR 10-SEP-1999; 99US-0153357.  
XX PR 26-JUL-2000; 2000US-0220947.  
XX PR 16-AUG-2000; 2000US-0225724.  
XX PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
PA (MILL-) MILLENNIUM PHARM INC.

XX PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;  
XX WPI: 2001-226749/23.

XX Nucleic acids comprising single nucleotide polymorphisms, useful in  
PT applications such as forensics, paternity testing, medicine, genetic  
PT analysis and phenotype correlations to diseases such as diabetes and  
PT atherosclerosis -  
XX Examples; Page 75; 242pp; English.  
XX The present invention provides a method of diagnosing a vascular disease  
CC in an individual, involving determining the sequence at various  
CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4  
genes. The sequences at a number of polymorphic sites are also provided  
CC in the specification. In particular, the method can be used in the  
CC diagnosis of atherosclerosis, myocardial infarction, coronary heart  
CC disease, stroke, peripheral vascular diseases, venous thromboembolism  
CC and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also  
CC useful in forensics, paternity testing, genetic analysis and phenotype  
CC correlations to diseases. The present sequence is an example of one of  
CC the human gene SNPs shown in the specification.  
XX Sequence 21 BP; 8 A; 4 C; 7 G; 2 T; 0 other;

CC the human gene SNPs shown in the specification.  
XX Sequence 21 BP; 3 A; 7 C; 6 G; 5 T; 0 other;

SQ Query Match 1.0%; Score 21; DB 22; Length 21;  
Best Local Similarity 100.0%; Pred. No. 6.3;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 507 acgcgttgcacttcggagac 527  
||||| ||||| |||||  
Db 1 ccgcgttgcacttcggagac 21

RESULT 14  
AAF95625  
ID AAF95625 standard; DNA; 21 BP.  
XX AC AAF95625;  
XX DT 06-JUN-2001 (first entry)

XX Human gene single nucleotide Polymorphism #386.  
DE Human; variant thrombospondin 1; variant thrombospondin 4; SNP;  
KW polymorphism; vascular disease; coronary artery disease; forensics;  
KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;  
KW pulmonary embolism; paternity test; ds.  
XX Homo sapiens.  
OS Homo sapiens.  
XX FH Key Variation  
FT Location/Qualifiers  
FT replace(11,T)  
FT /\*tag= a  
FT /standard\_name= "single nucleotide polymorphism"  
XX PN WO200118250-A2.  
XX PD 15-MAR-2001.  
XX PN 07-SEP-2000; 2000WO-US24503.  
XX PR 10-SEP-1999; 99US-0153357.  
PR 26-JUL-2000; 2000US-0220947.  
PR 16-AUG-2000; 2000US-0225724.  
XX PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
PA (MILL-) MILLENNIUM PHARM INC.

XX PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;  
XX WPI: 2001-226749/23.

XX Nucleic acids comprising single nucleotide polymorphisms, useful in  
PT applications such as forensics, paternity testing, medicine, genetic  
PT analysis and phenotype correlations to diseases such as diabetes and  
PT atherosclerosis -  
XX Examples; Page 75; 242pp; English.  
XX The present invention provides a method of diagnosing a vascular disease  
CC in an individual, involving determining the sequence at various  
CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4  
genes. The sequences at a number of polymorphic sites are also provided  
CC in the specification. In particular, the method can be used in the  
CC diagnosis of atherosclerosis, myocardial infarction, coronary heart  
CC disease, stroke, peripheral vascular diseases, venous thromboembolism  
CC and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also  
CC useful in forensics, paternity testing, genetic analysis and phenotype  
CC correlations to diseases. The present sequence is an example of one of  
CC the human gene SNPs shown in the specification.  
XX Sequence 21 BP; 8 A; 4 C; 7 G; 2 T; 0 other;

CC The present invention provides a method of diagnosing a vascular disease  
CC in an individual, involving determining the sequence at various  
CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4  
genes. The sequences at a number of polymorphic sites are also provided  
CC in the specification. In particular, the method can be used in the  
CC diagnosis of atherosclerosis, myocardial infarction, coronary heart  
CC disease, stroke, peripheral vascular diseases, venous thromboembolism  
CC and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also  
CC useful in forensics, paternity testing, genetic analysis and phenotype  
CC correlations to diseases. The present sequence is an example of one of  
CC the human gene SNPs shown in the specification.  
XX Sequence 21 BP; 8 A; 4 C; 7 G; 2 T; 0 other;

Query Match 1.0%; Score 21; DB 22; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 6.3;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 773 tggaccactacaagaaggga 793  
 Db 1 tggaccactacaagaaggga 21

RESULT 1.5  
 AAF95626  
 ID AAF95626 standard; DNA; 21 BP.  
 XX  
 AC AAF95626;  
 DT 06-JUN-2001 (first entry)  
 DE Human gene single nucleotide polymorphism #388.  
 XX  
 KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;  
 KW polymorphism; vascular disease; coronary artery disease; forensics;  
 KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;  
 KW pulmonary embolism; paternity test; ds.  
 OS Homo sapiens.  
 XX  
 FH Key Variation  
 FT Location/Qualifiers replace(11,T)  
 FT /standard\_name= "single nucleotide polymorphism"  
 FT /tag= a  
 FT /standard\_name= "single nucleotide polymorphism"  
 PN WO200118250-A2.  
 XX  
 PD 15-MAR-2001.  
 XX  
 PR 07-SEP-2000; 2000WO-US24503.  
 XX  
 PR 10-SEP-1999; 99US-0153357.  
 XX  
 PR 26-JUL-2000; 2000US-022047.  
 XX  
 PR 16-AUG-2000; 2000US-0225724.  
 PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;  
 XX  
 DR WPI: 2001-226749/23.  
 XX  
 PT Nucleic acids comprising single nucleotide polymorphisms, useful in  
 PT applications such as forensics, paternity testing, medicine, genetic  
 PT analysis and phenotype correlations to diseases such as diabetes and  
 PT atherosclerosis -  
 XX  
 PS Examples: Page 75; 242pp; English.  
 XX  
 CC The present invention provides a method of diagnosing a vascular disease  
 CC in an individual, involving determining the sequence at various  
 CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4  
 CC genes. The sequences at a number of polymorphic sites are also provided  
 CC in the specification. In particular, the method can be used in the  
 CC diagnosis of atherosclerosis, myocardial infarction, coronary heart  
 CC disease, stroke, peripheral vascular diseases, venous thromboembolism  
 CC and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also  
 CC useful in forensics, paternity testing, genetic analysis and phenotype  
 CC correlations to diseases. The present sequence is an example of one of  
 CC the human gene SNPs shown in the specification.  
 XX  
 SQ Sequence 21 BP; 2 A; 5 C; 6 G; 8 T; 0 other;  
 Query Match 1.0%; Score 21; DB 22; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 6.3;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 377 ccattcaccagaagactca 397  
DB 1 cccatcaccccgaaactca 21

RESULT 17  
AAF95628  
ID AAF95628 standard; DNA; 21 BP.  
XX  
AC AAF95628;  
XX DT 06-JUN-2001 (first entry)  
XX Human gene single nucleotide polymorphism #389.  
DE Human; variant thrombospondin 1; variant thrombospondin 4; SNP;  
KW polymorphism; vascular disease; forensics;  
XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;  
KW polymorphism; vascular disease; coronary artery disease; forensics;  
KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;  
KW pulmonary embolism; paternity test; ds.  
XX Homo sapiens.

OS Homo sapiens.  
XX Key Variation Location/Qualifiers  
FH FT replace(11,T) /standard\_name= "single nucleotide polymorphism"  
FT FT /\*tag= a  
FT FT replace(11,G) /standard\_name= "single nucleotide polymorphism"  
XX PN WO200118250-A2.  
PN WO200118250-A2.  
XX PD 15-MAR-2001.  
XX PP 07-SEP-2000; 2000WO-US24503.  
XX PD 15-MAR-2001.  
XX PF 07-SEP-2000; 2000WO-US24503.  
XX PR 10-SEP-1999; 99US-0153357.  
PR 26-JUL-2000; 2000US-020947.  
PR 16-AUG-2000; 2000US-0225724.  
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PA (MILL-) MILLENIUM PHARM INC.  
XX DR WPI; 2001-226749/23.  
XX RI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;  
XX DR WPI; 2001-226749/23.  
XX PT Nucleic acids comprising single nucleotide polymorphisms, useful in  
PT applications such as forensics, paternity testing, medicine, genetic  
PT analysis and phenotype correlations to diseases such as diabetes and  
PT atherosclerosis -  
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XX CC in an individual, involving determining the sequence at various  
CC CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4  
CC genes. The sequences at a number of polymorphic sites are also provided  
CC in the specification. In particular, the method can be used in the  
CC diagnosis of atherosclerosis, myocardial infarction, coronary heart  
CC disease, stroke, peripheral vascular diseases, venous thromboembolism  
CC and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also  
CC useful in forensics, paternity testing, genetic analysis and phenotype  
CC correlations to diseases. The present sequence is an example of one of  
CC the human gene SNPs shown in the specification.  
XX Sequence 21 BP; 4 A; 11 C; 4 G; 2 T; 0 other;

RESULT 18  
AAF95629  
ID AAF95629 standard; DNA; 21 BP.  
XX  
AC AAF95629;  
XX DT 06-JUN-2001 (first entry)  
XX Human gene single nucleotide polymorphism #390.  
DE Human; variant thrombospondin 1; variant thrombospondin 4; SNP;  
KW polymorphism; vascular disease; coronary artery disease; forensics;  
KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;  
KW pulmonary embolism; paternity test; ds.  
XX Homo sapiens.

OS Homo sapiens.  
XX Key Variation Location/Qualifiers  
FH FT replace(11,T) /standard\_name= "single nucleotide polymorphism"  
FT FT /\*tag= a  
XX PN WO200118250-A2.  
PN WO200118250-A2.  
XX PD 15-MAR-2001.  
XX PP 07-SEP-2000; 2000WO-US24503.  
XX PR 10-SEP-1999; 99US-0153357.  
PR 26-JUL-2000; 2000US-020947.  
PR 16-AUG-2000; 2000US-0225724.  
XX PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
PA (MILL-) MILLENIUM PHARM INC.  
XX PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;  
PA (MILL-) MILLENIUM PHARM INC.  
XX DR WPI; 2001-226749/23.  
XX RI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ;  
XX DR WPI; 2001-226749/23.  
XX PT Nucleic acids comprising single nucleotide polymorphisms, useful in  
PT applications such as forensics, paternity testing, medicine, genetic  
PT analysis and phenotype correlations to diseases such as diabetes and  
PT atherosclerosis -  
XX Examples; Page 75; 242PP; English.  
PS The present invention provides a method of diagnosing a vascular disease  
XX CC in an individual, involving determining the sequence at various  
CC CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4  
CC genes. The sequences at a number of polymorphic sites are also provided  
CC in the specification. In particular, the method can be used in the  
CC diagnosis of atherosclerosis, myocardial infarction, coronary heart  
CC disease, stroke, peripheral vascular diseases, venous thromboembolism  
CC and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also  
CC useful in forensics, paternity testing, genetic analysis and phenotype  
CC correlations to diseases. The present sequence is an example of one of  
CC the human gene SNPs shown in the specification.  
XX Sequence 21 BP; 4 A; 8 C; 8 G; 1 T; 0 other;

RESULT 19  
Query Match Score 21; DB 22; Length 21;  
Best Local Similarity 100.0%; Pred. No. 6 3;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Gaps 0;  
QY 230 ccagtgcggccacccactgtc 250  
Db 1 ccagtgcggccacccactgtc 21  
QY 461 ccctggccacccggaaagg 481  
Db 1 ccctggccacccggaaagg 21

AAFP95630  
 ID AAF95630 standard; DNA; 21 BP.  
 XX  
 AC AAF95630;  
 XX  
 DT 06-JUN-2001 (first entry)  
 DE Human gene single nucleotide polymorphism #391.  
 XX  
 KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;  
 KW polymorphism; vascular disease; coronary artery disease; forensics;  
 KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;  
 KW pulmonary embolism; paternity test; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Variation replace(1..1,T)  
 FT /\*tag= a  
 FT /standard\_name= "single nucleotide polymorphism"  
 XX  
 PN WO200118250-A2.  
 XX  
 PD 15-MAR-2001.  
 XX  
 PP 07-SEP-2000; 20000WO-US24503.  
 XX  
 PR 10-SEP-1999; 99US-0153357.  
 PR 26-JUL-2000; 20000US-0220947.  
 PR 16-AUG-2000; 20000US-0225724.  
 XX  
 PA (WHEID ) WHITEHEAD INST BIOMEDICAL RES.  
 PA (MILL-) MILLENIUM PHARM INC.  
 XX  
 PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ,  
 XX  
 DR WPI; 2001-22679/23.  
 XX  
 PT Nucleic acids comprising single nucleotide polymorphisms, useful in  
 PT analyses such as forensics, paternity testing, medicine, genetic  
 PT analysis and phenotype correlations to diseases such as diabetes and  
 PT atherosclerosis -  
 XX  
 PS Examples; Page 75; 242pp; English.  
 XX  
 CC The present invention provides a method of diagnosing a vascular disease  
 CC in an individual, involving determining the sequence at various  
 CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4  
 CC genes. The sequences at a number of polymorphic sites are also provided  
 CC in the specification. In particular, the method can be used in the  
 CC diagnosis of atherosclerosis, myocardial infarction, coronary heart  
 CC disease, stroke, peripheral vascular diseases, venous thromboembolism  
 CC and pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also  
 CC useful in forensics, paternity testing, genetic analysis and phenotype  
 CC correlations to diseases. The present sequence is an example of one of  
 CC the human gene SNPs shown in the specification.  
 XX  
 SQ Sequence 21 BP; 6 A; 9 C; 3 G; 3 T; 0 other;

Query Match 1.0%; Score 21; DB 22; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 6..3;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 384 ccacaaagactcaggcttcca 404  
 ||||| ||||| ||||| ||||| |||||  
 Db 1 ccacaaagactcaggcttcca 21

RESULT 21  
 AAT41208/C  
 ID AAT41208 standard; DNA; 20 BP.  
 XX  
 AC AAT41208;  
 XX  
 DT 03-DEC-1996 (first entry)  
 DE Human gene signature HUMGS01089-derived anti-sense primer.  
 KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;  
 KW human; cloning; mapping; non-biased library; diagnosis; detection;  
 KW cell typing; abnormal cell function; primer; PCR; amplification;

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KW	polymerase chain reaction; ss.	XX	PD 05-JUL-2001.
XX	Synthetic.	OS	XX
XX		PN WO9514772-A1.	XX
XX		PR 01-JUN-1995.	XX
PD		PR 11-NOV-1994;	XX
XX		PR 12-NOV-1993;	XX
XX		PA (MATS//) MATSUBARA K.	XX
PA (OKUB//)	OKUBO K.	PI Matsubara K,	XX
XX		PI Okubo K;	XX
XX		DR WPI, 1995-206931/27.	XX
XX		PT Identifying gene signatures in 3'-directed human cDNA library - e.g., PT for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human tissues	XX
XX	Example 7; Fig 8; 2245pp; Japanese;	PS	CC sequences which did not match with sequences deposited in Genbank release 76. The GS sequences (119001-T26837) were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types. The primers T41207-8 amplify clone pm0112 which comprises the GS RUMGS001089 (T20089), located on chromosome 20.
SQ	Sequence 20 BP; 2 A; 6 C; 4 G; 8 T; 0 other;	CC	Sequence 51 BP; 7 A; 14 C; 19 G; 11 T; 0 other;
Query Match Score 1.0%	DB 16; Length 20;	CC	Sequence 51 BP; 7 A; 14 C; 19 G; 11 T; 0 other;
Best Local Similarity 100.0%	Pred. No. 19;	CC	Sequence 51 BP; 7 A; 14 C; 19 G; 11 T; 0 other;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	AC	AC	AC
QY 1673 aacaggccatgtatggaa 1692	AC	AAL33024_C	AAL33024_C
Db 20 AACAGCAGCCATGTATGGAA 1	XX	ID AAL33024_C	ID AAL33024_C
DT 24-JAN-2002 (first entry)	XX	DE Human SNP oligonucleotide #6232.	DE Human SNP oligonucleotide #6233.
XX	DE Human SNP oligonucleotide #6232.	XX	KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic; neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer; amyloid protein; angiopoietin; apoptosis related protein; cathepsin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinesin; cytokine; interferon; interleukin; G-protein coupled receptor; thioesterase; inflammation; multifactorial disease; autoimmune disease; infection; nervous system disease; ss.
XX	OS Homo sapiens.	XX	OS Homo sapiens.
XX	NN WO200147944-A2.	XX	NN WO200147944-A2.
PN	PD 05-JUL-2001.	PD	PD 05-JUL-2001.

XX	28-DEC-2000;	2000WO-US35498.	PF	WPI; 2000-412314/35.
XX	28-DEC-1999;	99US-0173419.	PR	New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
XX	27-DEC-2000;	2000US-0173419.	PT	PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PA	(CURA -) CURAGEN CORP.	PA	PA PCNA and Cyclin B1 -	
XX	Shimkets RA, Leach M;	PI	PI Disclosure; Page 53; 109pp; English.	
XX	WPI; 2001-465210/50.	XX	XX The present invention relates to a hairpin or hammerhead ribozyme, designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase other than cell cycle dependent kinases CDK1, PCNA and Cyclin B1.	
XX	Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases, oncogenes and histones, useful for diagnosing and treating, e.g. autoimmune diseases and infections -	PT	CC Representative examples of ribozyme recognition sites are given in AAA82415 to AAA86787. The ribozyme of the invention is useful for inhibiting restenosis by introduction of the ribozyme into cells. The ribozyme is resistant to endonuclease activity and hence is efficient in restenosis treatment.	
XX	Claim 1; Page 3170; 4143pp; English.	XX	CC Sequence 19 BP; 1 A; 6 C; 7 G; 5 T; 0 other;	
XX	The present invention relates to oligonucleotides encoding polymorphic variants of proteins related to amyloids, amyloid proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes, histones, kinases, colony stimulating factors, complement related proteins, cytochromes, kinesins, cytokines, interleukins, G-protein coupled receptors and thioesterses. The present sequence is one such oligonucleotide and the peptides encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate expression of the proteins listed above. Disorders that may be prevented, diagnosed and/or treated include multifactorial diseases with a genetic component, such as autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus and Grave's disease), inflammation, cancer (e.g. cancers of the bladder, brain, breast, colon and kidney, leukaemia), diseases of the nervous system and an infection of pathogenic organisms.	CC	CC Query Match Score 0.9%; Best Local Similarity 100.0%; Pred. No. 1.9e-02; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Gaps	
XX	Sequence 51 BP; 7 A; 12 C; 20 G; 12 T; 0 other;	PS	XX Qy 1297 gctgactttggcgttggcc 1314 Db 2 gctgactttggcgttggcc 19	
XX	AAH58041 standard; DNA; 19 BP.	XX	XX RESULT 25 ID AAH58041 standard; DNA; 19 BP. AAH58041;	
XX	AAH58041;	AC	XX DT 10-SEP-2001 (first entry)	
XX	Cell -cycle dependent kinase cdk4 ribozyme binding site SEQ ID NO:465.	XX	XX DE Cell -cycle dependent kinase cdk4 ribozyme binding site SEQ ID NO:465.	
XX	Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme; skin disease; psoriasis; diabetic retinopathy; eye disease; vulnery; KW recognition site; target; ribozyme binding site; eye disease; vulnery; KW proliferative disease; skin disease; psoriasis; diabetic retinopathy; KW cytokine; inflammation; cell -cycle dependent kinase; cyclin; MMF; KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic; KW antipsoriatic; dermatological; antisborrelic; antidiabetic; virucide; KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart; KW atopic dermatitis; actinic keratos; squamous cell carcinoma; KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar; KW sickle cell retinopathy; ss.	XX	XX Homo sapiens.	
XX	OS Synthetic.	XX	XX OS Synthetic.	
XX	WO200130362-A2.	PN	XX PN WO200130362-A2.	
XX	03-MAY-2001.	PD	XX PD 03-MAY-2001.	
XX	26-OCT-2000; 2000WO-US29500.	PF	XX PF 26-OCT-2000; 2000WO-US29500.	
XX	PR 26-OCT-1999; 99US-0161532.	PR	XX PR 26-OCT-1999; 99US-0161532.	
XX	(IMMU -) IMMUSOL INC.	PA	XX PA (IMMU -) IMMUSOL INC.	
XX	Robbins JM, Tritz R;	PI	XX PI Robbins JM, Tritz R;	
XX	WPI; 2001-300427/31.	DR	XX DR WPI; 2001-300427/31.	
XX	Treating proliferative skin or eye diseases and scarring, using ribozymes that cleave RNA encoding cytokines involved in inflammation, matrix metalloproteinases, growth factors and cell-cycle dependent kinases -	PT	PT PT PT PT	
XX	(IMMU -) IMMUSOL INC.	PA	XX PA (IMMU -) IMMUSOL INC.	
XX	Tritz R, Welch DJ, Parbor TP	PT	XX PT Tritz R, Welch DJ, Parbor TP	

PS Example 1; Page 105; 400pp; English.  
 XX The present invention describes a method for treating a proliferative skin or eye disease and scarring. The method involves administering a ribozyme (I) which cleaves RNA encoding a cytokine involved in inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle dependent kinase, growth factor or reductase, or administering a nucleic acid molecule (II) comprising a promoter operably linked to a nucleic acid segment encoding (I). (I) can have antiproliferative, dermatological, cytostatic, antiseborrheic, antidiabetic, antiseizuring, ophthalmological, vulneral, keratolytic and virucidal activities, and cleaves RNA encoding cytokine involved in inflammation. (I) can be used in gene therapy. (I) and (II) are useful for treating proliferative skin diseases such as porokeratosis, atopic dermatitis, actinic keratosis, squamous or basal cell carcinoma and viral or seborrheic wart. They can also be used for treating proliferative eye diseases such as diabetic retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of prematurity and retinal detachment, and for treating and preventing scarring such as keloid adhesion and hypertrophic or hypertrophic burn exemplification of the present invention.

XX Sequence 19 BP; 1 A; 6 C; 7 G; 5 T; 0 other;

Query Match 0.9%; Score 18; DB 22; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1297 gctgacttggcctggcc 1314  
 Db 2 gctgacttggcctggcc 19

RESULT 26  
 AAX23342 standard; DNA; 20 BP.  
 ID AAX23342 standard; DNA; 20 BP.  
 XX  
 AC AAX23342;  
 XX DR 10-JUN-1999 (first entry)

Chemically modified sense control probe ISIS No: 14318.  
 DE  
 KW Antisense oligonucleotide; Jun N-terminal kinase; JNK; hybridise; JNK1;  
 KW JNK2; JNK; cell cycle progression; phosphorylation; probe;  
 KW hyperproliferative disease; human; ss.  
 OS Synthetic.  
 XX Homo sapiens.  
 PN WO9009214-A1.

XX DR 25-FEB-1999.  
 XX PR 07-AUG-1998; 98WO-US16488.  
 XX 13-AUG-1997; 97US-0910629.  
 PA (ISIS-) ISIS PHARM INC.

XX PI Dean N, Gaarde WA, McKay R, Monia BP, Nero PS;  
 XX DR 1999-181060/15.  
 XX PR 07-AUG-1998; 98WO-US16488.  
 XX PA (ISIS-) ISIS PHARM INC.

XX The invention relates to antisense oligonucleotides that detect and modulate the expression of Jun N-terminal kinase (JNK) proteins. The antisense oligonucleotides specifically hybridize to a nucleic acid encoding a JNK1, JNK2 or JNK3 protein, and which modulate expression of these proteins. The oligonucleotides are useful for modulating JNK protein expression of a cellular protein that has been phosphorylated by a JNK protein, and the expression of a cellular protein that promotes one or more metastatic events. The oligonucleotides also form pharmaceutical compositions for treating animals with a hyperproliferative disease, and for inhibiting tumor growth in an animal.

PS Example 1; Page 105; 400pp; English.  
 XX The present invention describes a method for treating a proliferative skin or eye disease and scarring. The method involves administering a ribozyme (I) which cleaves RNA encoding a cytokine involved in inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle dependent kinase, growth factor or reductase, or administering a nucleic acid molecule (II) comprising a promoter operably linked to a nucleic acid segment encoding (I). (I) can have antiproliferative, dermatological, cytostatic, antiseborrheic, antidiabetic, antiseizuring, ophthalmological, vulneral, keratolytic and virucidal activities, and cleaves RNA encoding cytokine involved in inflammation. (I) can be used in gene therapy. (I) and (II) are useful for treating proliferative skin diseases such as porokeratosis, atopic dermatitis, actinic keratosis, squamous or basal cell carcinoma and viral or seborrheic wart. They can also be used for treating proliferative eye diseases such as diabetic retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of prematurity and retinal detachment, and for treating and preventing scarring such as keloid adhesion and hypertrophic or hypertrophic burn exemplification of the present invention.

XX Sequence 20 BP; 2 A; 7 C; 7 G; 4 T; 0 other;

Query Match 0.9%; Score 18; DB 20; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1300 gacttggctggccgg 1317  
 Db 1 gacttggccctggcccg 18

RESULT 27  
 AAX2331/C  
 ID AAX2331 standard; DNA; 20 BP.  
 XX AC AAX2331;  
 XX DT 10-JUN-1999 (first entry)  
 XX DE JNK2-specific probe ISIS No: 12560.  
 XX KW Antisense oligonucleotide; Jun N-terminal kinase; JNK; hybridise; JNK1;  
 KW JNK2; JNK; cell cycle progression; phosphorylation; tumour; ss.  
 XX DE Synthetic.  
 OS Homo sapiens.  
 XX PN WO9009214-A1.  
 XX PD 25-FEB-1999.  
 XX XX 07-AUG-1998; 98WO-US16488.  
 XX PR 13-AUG-1997; 97US-0910629.  
 PA (ISIS-) ISIS PHARM INC.

XX PI Dean N, Gaarde WA, McKay R, Monia BP, Nero PS;  
 XX DR 1999-181060/15.  
 XX PT New antisense oligonucleotides that detect and modulate the expression of Jun N-terminal kinase proteins - useful for treating hyperproliferative diseases and inhibiting tumor growth in animals, and for modulating protein phosphorylation by these proteins

XX PS Example 4; Page 87; 190pp; English.  
 XX The invention relates to antisense oligonucleotides that detect and modulate the expression of Jun N-terminal kinase (JNK) proteins. The antisense oligonucleotides specifically hybridize to a nucleic acid encoding a JNK1, JNK2 or JNK3 protein, and which modulate expression of these proteins. The oligonucleotides are useful for modulating JNK protein expression of a cellular protein that has been phosphorylated by a JNK protein, and the expression of a cellular protein that promotes one or more metastatic events. The oligonucleotides also form pharmaceutical compositions for treating animals with a hyperproliferative disease, and for inhibiting tumor growth in an animal.

CC tumor growth in an animal.  
 XX Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;

Query Match Local Similarity 0.98; Score 18; DB 20; Length 20;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1300 gacttggcctggccgg 1317  
 ||||| | | | | | | | | | | |  
 Db 20 GACTTGGCCTGGCCGG 3

RESULT 29  
 AAC62885 standard; DNA; 20 BP.  
 ID AAC62885  
 XX AC AAC62885;  
 XX DT 06-FEB-2001 (first entry)  
 XX DE JNK antisense oligonucleotide ISIS #14318.  
 XX KW Antisense; gene therapy; JNK2 protein; apoptosis; cancer;  
 XX KW cellular hyperproliferation; Alzheimer's; Parkinson's disease;  
 AC amyotrophic lateral sclerosis; retinitis; pigmentosa; epilepsy;  
 XX KW myocardial infarction; stroke; obstructive jaundice; polycystic kidney;  
 KW diabetes; Jun N-terminal kinase; ss.  
 XX OS Homo sapiens.  
 XX PN WO200059549-A1.  
 XX PD 12-OCT-2000.  
 XX PF 04-APR-2000; 2000WO-US08880.  
 XX PR 07-APR-1999; 99US-0287796.  
 XX PA (ISIS-) ISIS PHARM INC.  
 XX PI McKay R, Dean NM, Monia BP, Nero PS, Gaarde WA;  
 XX DR WOI; 2000-638427/61.  
 XX PT Novel methods for reducing apoptosis comprising contacting cells with antisense oligonucleotides, useful for treating apoptotic disorders,  
 PT e.g. cancer -  
 XX PR Example 4; Page 135; 160pp; English.  
 XX PS (ISIS-) ISIS PHARM INC.  
 XX PI McKay R, Dean NM, Monia BP, Nero PS, Gaarde WA;  
 XX DR WPI; 2000-638427/61.  
 PT Novel methods for reducing apoptosis comprising contacting cells with antisense oligonucleotides, useful for treating apoptotic disorders,  
 PT e.g. cancer -  
 XX PR Claim 3; Page 133; 160pp; English.  
 XX CC The present invention relates to antisense oligonucleotides (AAC6284-C63000, AAA96093-A96099 and AAA07993) that hybridise specifically to a nucleotide encoding a Jun N-terminal kinase (JNK2) protein, resulting in decrease of JNK2 expression and leading to induction of apoptosis. The present sequence is one such antisense oligonucleotide. The oligonucleotides of the present invention are useful for treating diseases or conditions with reduced apoptosis, e.g. cancer and cellular hyperproliferation. The oligonucleotides may also be used to increase the stimulation of apoptotic proteins, e.g. for treating Alzheimer's or Parkinson's disease, amyotrophic lateral sclerosis, retinitis, pigmentosa, epilepsy, myocardial infarction, stroke, obstructive jaundice, polycystic kidney and diabetes. The present sequence may have a phosphorothioate backbone.  
 XX SQ Sequence 20 BP; 2 A; 7 C; 7 G; 2 T; 0 other;

Query Match Local Similarity 0.9%; Score 18; DB 21; Length 20;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1300 gacttggcctggccgg 1317  
 ||||| | | | | | | | | | | |  
 Db 1 gacttggcctggccgg 18

RESULT 30  
 AAA48651/C  
 ID AAA48651 standard; DNA; 20 BP.  
 XX

AC AAA48651;  
 XX DT 20-SEP-2000 (first entry)  
 DE Antisense oligonucleotide ISIS no.15354 to human JNK2 gene.  
 XX KW Antisense; E-selectin; TNF alpha; cell adhesion;  
 KW tumour necrosis factor alpha; phosphorothioate; methoxyethoxy;  
 KW sepsis; rheumatoid arthritis; inflammatory disease;  
 KW inflammatory bowel disease; allergic contact dermatitis; psoriasis;  
 KW diabetes; Grave's disease; allograft rejection; cancer; antibacterial;  
 KW immunosuppressive; antipsoriatic; antidiabetic; antithyroid;  
 KW cytostatic; dermatological; antiallergic; Ha-ras; c-raf;  
 KW c-jun N-terminal kinase; JNK; ss.  
 XX OS Homo sapiens.  
 XX Key modified\_base Location/Qualifiers  
 FT 1..6 /\*tag= a  
 FT /mod\_base= OTHER  
 FT /\*note= "All bases are 2'-methoxyethoxy,  
 FT additionally C bases are m5c"  
 FT 7..15 /\*tag= b  
 FT /mod\_base= OTHER  
 FT /\*note= "Phosphorothioate internucleotide linkage"  
 FT 16..20 /\*tag= C  
 FT /mod\_base= OTHER  
 FT /\*note= "All bases are 2'-methoxyethoxy,  
 FT additionally C bases are m5c"  
 XX PN WO2000034303-A1.  
 XX PD 15-JUN-2000.  
 XX PF 08-DEC-1999; 99WO-US28965.  
 XX PR 10-DEC-1998; 98US-0209668.  
 XX PA (ISIS-) ISIS PHARM INC.  
 XX PI Monia BP, xu XS;  
 XX DR; 2000-423367/36.  
 XX PT Modulating cell adhesion molecule expression for treating immune or  
 PT inflammatory diseases involves treating cell with specific inhibitor of  
 PT Tumour Necrosis Factor alpha signalling molecule -  
 XX PS Claim 36; Page 46; 100pp; English.  
 XX A novel method for modulating cell adhesion molecule expression  
 CC involves antisense inhibition of a tumour necrosis factor (TNF) alpha  
 CC signalling molecule. In the method TNF alpha signalling molecules  
 CC Hsras, c-ras and c-jun N-terminal kinase (JNK)2 were inhibited by  
 CC antisense oligonucleotides. In addition an antisense oligonucleotide  
 CC to the cell adhesion molecule E-selectin was also examined. The  
 CC present sequence is the JNK2 antisense oligonucleotide. The  
 CC antisense oligonucleotides used in the method contained modifications,  
 CC namely phosphorothioate linkages and 2' methoxyethoxy bases. Some C  
 CC residues also had a 5'methyl modification. Inhibitors of the TNF alpha  
 CC signalling molecules have antibacterial, immunosuppressive,  
 CC antipsoriatic, antithyroid, cytostatic, dermatological,  
 CC antiallergic and antiinflammatory activity. The antisense inhibitors  
 CC may be useful for the treatment of sepsis, rheumatoid arthritis,  
 CC contact dermatitis, immune disease, inflammatory bowel disease, allergic  
 CC rejection and cancer.  
 XX SQ Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;

Query Match 0.9%; Score 18; DB 21; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1300 gacttggctggccgg 1317  
 AAH23754/C  
 ID AAH23754 standard; DNA; 20 BP.  
 Db 20 GACTTGGCTGGCCGG 3

RESULT 31

XX 13-AUG-2001 (first entry)  
 XX DE JNK1 antisense oligonucleotide, JNK2AS, (ISIS #12560).  
 KW JNK; jun kinase; antisense; cytostatic; cancer;  
 KW 2'-O-methoxyethyl oligonucleotide; MOE; phosphorothioate; ss.  
 XX OS Synthetic.  
 XX Key modified\_base Location/Qualifiers  
 FT 1..20 /\*tag= a  
 FT /mod\_base= "OTHER"  
 FT /\*note= "This oligonucleotide is a 2'-O-methoxyethyl (MOE)  
 FT chimeric antisense oligonucleotide containing five  
 FT MOE/phosphodiester residues flanking a  
 FT 2'-deoxynucleotide/phosphorothioate region"  
 FT WO200134792/A2.  
 XX PN 99US-0165224.  
 XX PD 17-MAY-2001.  
 XX PF 10-NOV-2000; 2000WO-US30869.  
 XX PR 12-NOV-1999; 99US-0165224.  
 XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX PI Potapova O, Gorospo M, Holbrook NJ;  
 XX DR; 2001-335925/35.  
 XX PT Use of Jun Kinase antisense mRNA for treating cancer by administering  
 PT vector comprising promoter operably linked to DNA sequence that encodes  
 PT the antisense mRNA to patient diagnosed with cancer -  
 XX PS Claim 1; Page 41; 75pp; English.  
 XX The present invention relates to the use of Jun Kinase (JNK) antisense  
 CC oligonucleotides for treating cancer and for screening compounds that  
 CC mimic or augment the effect of JNK antisense oligonucleotides treatment  
 CC for cancer. The present sequence is one such JNK antisense  
 CC oligonucleotide.  
 XX SQ Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;  
 Query Match 0.9%; Score 18; DB 22; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1300 gacttggctggccgg 1317  
 AAH23754/C  
 ID AAH23754 standard; DNA; 20 BP.  
 Db 20 GACTTGGCTGGCCGG 3

RESULT 32

AAF99183/C ID AAF99183 standard; DNA; 20 BP. XX AC AAF99183; XX DT 12-JUN-2001 (first entry) XX DE Immunostimulatory nucleic acid #299. XX Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic; KW immunostimulatory; tumour; viral infection; bacterial infection; KW fungal infection; parasitic infection; cancer; asthma; KW infectious disease; allergy; immune deficiency; phosphorothioate; ss. OS Homo sapiens. XX PN WO200132869-A1. XX PD 05-ABR-2001. XX Synthetic. XX PN WO200122972-A2. XX PS 05-ABR-2001. XX PF 25-SEP-2000; 2000WO-US26383. XX PR 25-SEP-1999; 99US-0156113. PR 27-SEP-1999; 99US-0156135. PR 23-AUG-2000; 2000US-022436. XX PA (IOWA ) UNIV IOWA RES FOUND. (COLE-) COLEY PHARM GMBH. XX PI Krieg AM, Schetter C, Volmer J; XX DR WPI; 2001-273485/28. XX PT Vaccinating against tumors, infectious diseases, allergies and asthma PT using immunostimulatory Py-rich and TG nucleic acids - XX Claim 101; Page 44; 338pp; English. XX The present invention relates to a method for stimulating an immune CC response. The method comprises administering an immunostimulatory nucleic CC acid to a non-rodent subject in sufficient quantity to stimulate an CC immune response. The present sequence is one such immunostimulatory CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects against tumor antigens, viral antigens (e.g. herpesviridae, retroviridae CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma, haemophilus, campylobacter, clostridium, Escherichia coli and/or staphylococcus), fungal antigens and/or parasitic antigens. The method is also useful for preventing cancer, asthma, infectious disease, allergy or immune deficiency. The present sequence can also be used to redirect a Th2 to a Th1 immune response and to activate immune cells. Note: the present sequence may have a phosphorothioate backbone. XX Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 other;	DE Human tyrosine kinase Hck PCR primer SEQ ID NO:9. XX KW Human; tyrosine kinase Hck binding protein; tyrosine kinase; Hck; AC KW tumour lethal factor; tumour necrosis factor alpha; apoptosis; HSB-1; KW Hck signal transduction; human immunodeficiency virus; HIV infection; KW anticancer; PCR primer; ss. XX OS Homo sapiens. XX PN WO200132869-A1. XX PD 10-MAY-2001. XX PP 26-OCT-2000; 2000WO-JP07500. XX PR 29-OCT-1999; 99JP-0309957. XX PA (SSSE ) SSP CO LTD. XX PI Taniyama T, Narita T; XX WPI; 2001-316440/33. XX DR XX PT New proteins which bind to human tyrosine kinase Hck for promotion of PT apoptosis and for the elucidation of the mechanism of Hck signal transduction - XX PS Example 3; Page 33; 45pp; Japanese. XX CC The present invention describes a protein, designated HSB-1, which binds CC to human tyrosine kinase Hck. Also described are: (1) nucleic acids CC encoding the protein and its derivatives; (2) recombinant vectors CC containing the nucleic acids; and (3) host cells transformed by the CC vectors and expressing the protein. HSB-1 has cytosolic activity and promotes CC apoptosis. HSB-1 enhances tumour necrosis factor alpha and promotes CC Hck signal transduction and of the role of Hck in human CC treatment of infections and other diseases with which Hck is associated. CC They promote the anticancer activity of tumour necrosis factor alpha. CC Hck signal transduction and of the role of Hck in human CC immunodeficiency virus (HIV) infection. They can be used for the CC elucidation of the mechanism of Hck in human CC disease. The present sequence represents a PCR primer for the human tyrosine CC kinase Hck, which is used in an example from the present invention. XX SQ Sequence 34 BP; 8 A; 8 C; 9 G; 9 T; 0 other; XX SQ Query Match Score 0.9%; Score 18; DB 22; Length 34; Best Local Similarity 100.0%; Pred. No. 1.9e+02; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0; XX ID AAA82878 standard; DNA; 19 BP. AC AAA82878; XX DT 04-DEC-2000 (first entry) XX OS Mammalia. DE CDK4 ribozyme binding site #59. XX KW Ribozyme; hairpin; hammerhead; gene therapy; vasotroptc; KW restenosis; ss. XX OS XX PN WO200032765-A2. XX PD 08-JUN-2000.
RESULT 33 AAH41497 ID AAH41497 standard; DNA; 34 BP. XX AC AAH41497; XX DT 23-AUG-2001 (first entry) XX	RESULT 34 AAA82878 ID AAA82878 standard; DNA; 19 BP. AC AAA82878; XX DT 04-DEC-2000 (first entry) XX OS Mammalia. DE CDK4 ribozyme binding site #59. XX KW Ribozyme; hairpin; hammerhead; gene therapy; vasotroptc; KW restenosis; ss. XX OS XX PN WO200032765-A2. XX PD 08-JUN-2000.
Qy 1300 gacttggctggccgg 1317 Db 20 GACTTGGCTGGCCGG 3	Qy 178 atgaaatccaaatgttcctc 195 Db 17 atgaaatccaaatgttcctc 34





GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on:

May 17, 2002, 16:26:59 : Search time 90.41 Seconds

(without alignments)  
5474.522 Million cell updates/sec

Title: US-10-007-010-3

Perfect score: 2015  
Sequence: 1 cggaggcacgaaatggatggg.....ataataatgcaagtcttacg 2015

Scoring table: OLIGO\_NUC

Gapext 60.0 , Gapext 60.0

Searched: 383533 seqs., 122816752 residues

Word size :

Total number of hits satisfying chosen parameters: 615614

Minimum DB seq length: 0

Maximum DB seq length: 105

Post-processing: Listing first 65 summaries

Database : Issued\_Patents.NA,\*

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2: /cgn2\_6/pctodata/2/ina/5B..COMB.seq,\*

3: /cgn2\_6/pctodata/2/ina/5A..COMB.seq,\*

4: /cgn2\_6/pctodata/2/ina/6B..COMB.seq,\*

5: /cgn2\_5/pctodata/2/ina/pcut5..COMB.seq,\*

6: /cgn2\_6/pctodata/2/ina/backfile1..seq,\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
c 1	18	0.9	20 2 US-08-910-029A-31	Sequence 31, Appl
c 2	18	0.9	20 2 US-08-910-029A-42	Sequence 42, Appl
c 3	18	0.9	20 3 US-09-209-668-7	Sequence 7, Appl
c 4	18	0.9	20 3 US-09-387-796-31	Sequence 31, Appl
c 5	18	0.9	20 3 US-09-387-796-42	Sequence 42, Appl
c 6	18	0.9	20 4 US-09-130-616-31	Sequence 31, Appl
c 7	18	0.9	20 4 US-09-130-616-42	Sequence 42, Appl
c 8	17	0.8	20 2 US-08-730-876-2	Sequence 2, Appl
c 9	17	0.8	20 4 US-09-490-592-71	Sequence 71, Appl
c 10	17	0.8	23 1 US-08-22-616-2	Sequence 2, Appl
c 11	17	0.8	23 5 PCT-US5-04228-2	Sequence 2, Appl
c 12	16	0.8	24 2 US-08-859-598	Sequence 598, App
c 13	16	0.8	24 4 US-09-225-938-598	Sequence 598, App
c 14	15	0.7	18 4 US-08-384-040-6218	Sequence 6218, Ap
c 15	15	0.7	19 1 US-08-400-580A-11	Sequence 11, Appl
c 16	15	0.7	19 2 US-08-932-23-51	Sequence 51, Appl
c 17	15	0.7	36 3 US-08-931-923-52	Sequence 52, Appl
c 18	15	0.7	36 3 US-08-724-386-3	Sequence 3, Appl
c 19	15	0.7	36 4 US-09-421-612-3	Sequence 3, Appl
c 20	15	0.7	45 2 US-08-039-198B-3	Sequence 47, Appl
c 21	15	0.7	72 2 US-08-107-337A-47	Sequence 19, Appl
c 22	15	0.7	104 3 US-09-058-389A-19	Sequence 78, Appl
c 23	15	0.7	105 4 US-09-461-637-78	Sequence 661, Ap
c 24	15	0.7	17 1 US-08-105-483-197	Sequence 197, Ap
c 25	14	0.7	18 1 US-08-220-151-78	Sequence 78, Ap
c 26	14	0.7		
c 27	14	0.7		

#### ALIGNMENTS

RESULT 1  
US-08-910-629A-31/C

Sequence 31, Application US/08910629A  
Patent No. 5877309  
GENERAL INFORMATION:  
APPLICANT: Robert A. McKay  
APPLICANT: Nicholas M. Dean  
APPLICANT: Brett Monia  
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS FOR THE MODULATION OF JNK PROTEINS  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Jane Massey Licata  
STREET: 66 East Main Street  
CITY: Marlton  
STATE: NJ  
COUNTRY: USA  
ZIP: 08053  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB  
COMPUTER: PENTIUM  
OPERATING SYSTEM: WINDOWS 95  
SOFTWARE: WORDPERFECT 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/910,629A  
FILING DATE: August 13, 1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:

APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jane Massey Licata  
; REGISTRATION NUMBER: 32,257  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (609) 779-2400  
; TELEFAX: (609) 779-8488  
; INFORMATION FOR SEQ ID NO: 31:  
; LENGTH: 20  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; ANTI-SENSE: Yes  
; US-08-910-629A-31

RESULT 3  
; ANTI-SENSE: No  
; US-08-910-629A-42  
Query Match Score 0.9%; Score 18; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1300 gacttggctggcccg 1317  
Db 1 GACTTGGCTGGCCCG 18

RESULT 3  
; ANTI-SENSE: No  
; Sequence 7, Application US-09209668A  
; Patent No. 6116517  
; GENERAL INFORMATION:  
; APPLICANT: Monia, Brett P.  
; TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR EXPRESSION OF CELL ADHESION MOLECULES  
; FILE REFERENCE: ISPH-0386  
; CURRENT APPLICATION NUMBER: US/09/209,668A  
; CURRENT FILING DATE: 1998-12-10  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: antisense sequence  
; US-09-209-668-7

RESULT 2  
; ANTI-SENSE: No  
; Sequence 42, Application US/08910629A  
; Patent No. 5877309  
; GENERAL INFORMATION:  
; APPLICANT: Robert A. McKay  
; APPLICANT: Nicholas M. Dean  
; APPLICANT: Brett Monia  
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS FOR THE MODULATION OF JNK PROTEINS  
; TITLE OF INVENTION: PROTEINS  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Law Offices of Jane Massey Licata  
; STREET: 66 East Main Street  
; CITY: Marlton  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 08053  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB  
; COMPUTER: PENTIUM  
; OPERATING SYSTEM: WINDOWS 95  
; SOFTWARE: WORDPERFECT 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/910,629A  
; FILING DATE: August 13, 1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jane Massey Licata  
; REGISTRATION NUMBER: 32,257  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (609) 779-2400  
; TELEFAX: (609) 779-8488  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear

RESULT 4  
; ANTI-SENSE: No  
; Sequence 31, Application US/09287796A  
; Patent No. 6133246  
; GENERAL INFORMATION:  
; APPLICANT: Robert A. McKay  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Nero, Pam  
; APPLICANT: Carde, William A.  
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS FOR THE MODULATION OF JNK PROTEINS  
; FILE REFERENCE: ISPH-0350  
; CURRENT APPLICATION NUMBER: US/09/287,796A  
; CURRENT FILING DATE: 1999-04-07  
; EARLIER APPLICATION NUMBER: 09/130,616  
; EARLIER FILING DATE: 1998-08-07  
; EARLIER APPLICATION NUMBER: 08/910,629  
; EARLIER FILING DATE: 1997-08-03  
; NUMBER OF SEQ ID NOS: 165  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
; US-09-287-796-31

Query Match 0.9%; Score 18; DB 3; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 23;  
 Matches 18; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Query Match 0.9%; Score 18; DB 4; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 23;  
 Matches 18; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1300 gacttgcgtggcccg 1317  
 Db 20 GACTTGCCTGGCCGG 3

RESULT 5  
 US-09-287-796-42  
 ; Sequence 42, Application US/09287796A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: McKay, Robert A.  
 ; APPLICANT: Dean, Nicholas M.  
 ; APPLICANT: Nero, Pam  
 ; APPLICANT: Gaarde, William A.  
 ; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS  
 ; FILE REFERENCE: ISPH-0350  
 ; CURRENT APPLICATION NUMBER: US/09/287,796A  
 ; CURRENT FILING DATE: 1999-04-07  
 ; EARLIER APPLICATION NUMBER: 09/130,616  
 ; EARLIER FILING DATE: 1998-08-07  
 ; EARLIER APPLICATION NUMBER: 08/910,629  
 ; EARLIER FILING DATE: 1997-08-03  
 ; NUMBER OF SEQ ID NOS: 165  
 ; SEQ ID NO 42  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic Sequence  
 US-09-287-796-42

Query Match 0.9%; Score 18; DB 3; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 23;  
 Matches 18; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Query Match 0.9%; Score 18; DB 4; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 23;  
 Matches 18; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1300 gacttgcgtggcccg 1317  
 Db 1 gacttgcgtggcccg 18

RESULT 6  
 US-09-130-616-31/C  
 ; Sequence 31, Application US/09130616C  
 ; GENERAL INFORMATION:  
 ; APPLICANT: McKay, Robert A.  
 ; APPLICANT: Dean, Nicholas M.  
 ; APPLICANT: Nero, Pam  
 ; APPLICANT: Gaarde, William A.  
 ; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS  
 ; FILE REFERENCE: ISPH-0318  
 ; CURRENT APPLICATION NUMBER: US/09/130,616C  
 ; CURRENT FILING DATE: 1998-08-07  
 ; EARLIER APPLICATION NUMBER: 08/910,629  
 ; EARLIER FILING DATE: 1997-08-03  
 ; NUMBER OF SEQ ID NOS: 178  
 ; SEQ ID NO 31  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic Sequence  
 US-09-130-616-42

Query Match 0.9%; Score 18; DB 4; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 23;  
 Matches 18; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Query Match 0.9%; Score 18; DB 4; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 23;  
 Matches 18; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1300 gacttgcgtggcccg 1317  
 Db 1 gacttgcgtggcccg 18

RESULT 7  
 US-09-130-616-42/C  
 ; Sequence 42, Application US/09130616C  
 ; Patent No. 6221850  
 ; GENERAL INFORMATION:  
 ; APPLICANT: McKay, Robert A.  
 ; APPLICANT: Dean, Nicholas M.  
 ; APPLICANT: Nero, Pam  
 ; APPLICANT: Gaarde, William A.  
 ; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS  
 ; TITLE OF INVENTION: FOR THE MODULATION OF JNK PROTEINS  
 ; FILE REFERENCE: ISPH-0318  
 ; CURRENT APPLICATION NUMBER: US/09/130,616C  
 ; CURRENT FILING DATE: 1998-08-07  
 ; EARLIER APPLICATION NUMBER: 08/910,629  
 ; EARLIER FILING DATE: 1997-08-03  
 ; SEQ ID NO 42  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic Sequence  
 US-09-130-616-42

Query Match 0.9%; Score 18; DB 4; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 23;  
 Matches 18; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Query Match 0.9%; Score 18; DB 4; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 23;  
 Matches 18; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1300 gacttgcgtggcccg 1317  
 Db 1 gacttgcgtggcccg 18

RESULT 8  
 US-08-730-876-2/C  
 ; Sequence 2, Application US/08730876  
 ; Patent No. 5859314  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hibbs, Margaret L.;  
 ; APPLICANT: Dunn, Ashley R.;  
 ; APPLICANT: Gratt, Dianne;  
 ; APPLICANT: Hodson, George;  
 ; APPLICANT: Tarlington, David M.;  
 ; APPLICANT: Armes, Jane  
 ; TITLE OF INVENTION: ANIMALS WITH TARGETED GENE DELETION  
 ; NUMBER OF SEQUENCES: 7  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Felfe & Lynch  
 ; STREET: 805 Third Avenue  
 ; CITY: New York City  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10022  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 3.5 inch, 1.44mb  
 ; COMPUTER: IBM PS/2  
 ; OPERATING SYSTEM: PC-DOS  
 ; SOFTWARE: Wordperfect  
 ; CURRENT APPLICATION DATA:

Query Match 0.9%; Score 18; DB 4; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 23;  
 Matches 18; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Query Match 0.9%; Score 18; DB 4; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 23;  
 Matches 18; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1300 gacttgcgtggcccg 1317  
 Db 1 gacttgcgtggcccg 18

RESULT 9  
 US-08-730-876-2/C  
 ; Sequence 2, Application US/08730876  
 ; Patent No. 5859314  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hibbs, Margaret L.;  
 ; APPLICANT: Dunn, Ashley R.;  
 ; APPLICANT: Gratt, Dianne;  
 ; APPLICANT: Hodson, George;  
 ; APPLICANT: Tarlington, David M.;  
 ; APPLICANT: Armes, Jane  
 ; TITLE OF INVENTION: ANIMALS WITH TARGETED GENE DELETION  
 ; NUMBER OF SEQUENCES: 7  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Felfe & Lynch  
 ; STREET: 805 Third Avenue  
 ; CITY: New York City  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10022  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 3.5 inch, 1.44mb  
 ; COMPUTER: IBM PS/2  
 ; OPERATING SYSTEM: PC-DOS  
 ; SOFTWARE: Wordperfect  
 ; CURRENT APPLICATION DATA:

Query Match 0.9%; Score 18; DB 4; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 23;  
 Matches 18; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Query Match 0.9%; Score 18; DB 4; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 23;  
 Matches 18; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1300 gacttgcgtggcccg 1317  
 Db 1 gacttgcgtggcccg 18

RESULT 10  
 US-09-130-616-31/C  
 ; Sequence 31, Application US/09130616C  
 ; GENERAL INFORMATION:  
 ; APPLICANT: McKay, Robert A.  
 ; APPLICANT: Dean, Nicholas M.  
 ; APPLICANT: Nero, Pam  
 ; APPLICANT: Gaarde, William A.  
 ; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS  
 ; FILE REFERENCE: ISPH-0318  
 ; CURRENT APPLICATION NUMBER: US/09/130,616C  
 ; CURRENT FILING DATE: 1998-08-07  
 ; EARLIER APPLICATION NUMBER: 08/910,629  
 ; EARLIER FILING DATE: 1997-08-03  
 ; NUMBER OF SEQ ID NOS: 178  
 ; SEQ ID NO 31  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Synthetic Sequence  
 US-09-130-616-31

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; APPLICATION NUMBER: US/08/730,876
; FILING DATE: 18-Oct-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,578
; FILING DATE: 20-oct-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 559314man D. Hanson
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5369 - JEL/NDH/SLH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-5200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-730-876-2

Query Match          0.8%; Score 17; DB 2; Length 20;
Best Local Similarity 100%; Pred. No. 72;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  916 gggcagtggaaagt 932
Db- 17 GGGCAGTTGGGAAGT 1

RESULT 9
US-09-490-692-71/c
; Sequence 71, Application US/09490692
; Patent No. 6180353
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; ATTORNEY: Lex M. Covert
; TITLE OF INVENTION: ANTISENSE MODULATION OF DAXX EXPRESSION
; FILE REFERENCE: RTIS-0120
; CURRENT APPLICATION NUMBER: US/09/490,692
; CURRENT FILING DATE: 2000-01-24
; SEQ ID NO 71
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-490-692-71

Query Match          0.8%; Score 17; DB 4; Length 20;
Best Local Similarity 100%; Pred. No. 72;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  28 tcaggaggatgtaaag 44
Db- 18 TCAGGAGATGTAAAG 2

RESULT 10
US-08-222-616-2/c
; Sequence 2, Application US/08222616
; Patent No. 5651177
; GENERAL INFORMATION:
; APPLICANT: Bennett, Brian D.
; APPLICANT: Goeddel, David
; APPLICANT: Lee, James M.
; APPLICANT: Matthews, William
; APPLICANT: Tsai, Siao Ping
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible

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RESULT 14  
 Qy 1236 catccaccggagaccc 1251  
 Db 8 CATCCACCGAGACCTC 23

US-08-951-923-51/c  
 Sequence 51, Application US/08951923

GENERAL INFORMATION:  
 APPLICANT: Blitter, Grant  
 TITLE OF INVENTION: PHENOTYPIC ASSAYS OF CYCLIN/CYCLIN-DEPENDENT KINASE

TITLE OF INVENTION: FUNCTION  
 NUMBER OF SEQUENCES: 57

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Cooley Godward LLP  
 STREET: 5 Palo Alto Square, 3000 El Camino Real  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: US

ZIP: 94306-2155  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/951-923  
 FILING DATE: October 16, 1997  
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
 NAME: Neely, Richard L.  
 REGISTRATION NUMBER: 30,092  
 REFERENCE/DOCKET NUMBER: BIRT-001/02US

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650 843-5000  
 TELEFAX: 650 857-0663  
 TELEX: 380816COOLEYPA

INFORMATION FOR SEQ ID NO: 51:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 18  
 TYPE: nucleic acid  
 STRANDEDNESS: single stranded  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO

US-08-951-923-51

Query Match Score 15; DB 3; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1300 gacttggctggcc 1314  
 Db 18 GACTTGGCTGGCC 4

RESULT 15  
 US-08-584-040-6218/c  
 Sequence 6218, Application US/08584040

GENERAL INFORMATION:  
 APPLICANT: Pavco, Pamela  
 APPLICANT: MoSwigen, James  
 APPLICANT: Stinchcomb, Dan T.  
 APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
 TITLE OF INVENTION: TREATMENT OF DISEASES OR LEVELS  
 TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS  
 TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL

; TITLE OF INVENTION: GROWTH FACTOR  
 ; NUMBER OF SEQUENCES: 8502  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071-2066  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; SOFTWARE: Word Perfect 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/584,040  
 ; FILING DATE: January 11, 1996  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 60/005,974  
 ; FILING DATE: October 26, 1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warburg, Richard J.  
 ; REGISTRATION NUMBER: 32,327  
 ; REFERENCE/DOCKET NUMBER: 218/064  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (213) 489-1600  
 ; TELEFAX: (213) 955-0440  
 ; TELEX: 67-3510  
 ; INFORMATION FOR SEQ ID NO: 6218:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 18 base Pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-584-040-6218

Query Match Score 15; DB 4; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 666 cgaccctcgccagg 680  
 Db 18 CGACCCCTGGCAGGG 4

RESULT 16  
 US-08-400-580A-11  
 Sequence 11, Application US/08400580A  
 ; Patent No. 5633501  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lee, Chao-Hung  
 ; APPLICANT: Jiang, Bingdong  
 ; TITLE OF INVENTION: Compounds and Methods To Determine  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Kristine H. Johnson  
 ; STREET: 123 No. 5693501th College Ave, Ste 213  
 ; CITY: Fort Collins  
 ; STATE: CO  
 ; COUNTRY: USA  
 ; ZIP: 80524  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/400,580A

FILING DATE: 08-MAR-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Johnson, Kristine H.  
 REGISTRATION NUMBER: 36,835  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (970) 472-9650  
 TELEFAX: (970) 472-9555  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 19 base Pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: RNA  
 US-08-400-580A-11

Query Match 0.7%; Score 15; DB 2; Length 31;  
 Best Local Similarity 100.0%; Pred. No. 7.2e-02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

---

RESULT 18  
 US-08-951-923-52  
 ; Sequence 52 Application US/08951923  
 ; Patent No. 6018693  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bitter, Grant  
 ; INVENTION: PHENOTYPIC ASSAYS OF CYCLIN/CYCLIN-DEPENDENT KINASE  
 ; TITLE OF INVENTION: FUNCTION  
 ; NUMBER OF SEQUENCES: 57  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Cooley Godward LLP  
 ; STREET: 5 Palo Alto Square, 3000 El Camino Real  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: US  
 ; ZIP: 94306-2155  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/951,923  
 FILING DATE: October 16, 1997  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Neeley, Richard L.  
 REGISTRATION NUMBER: 30,092  
 REFERENCE DOCKET NUMBER: BIRT-001/02US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650 843-5000  
 TELEFAX: 650 857-0663  
 TELEX: 38081GOOLEYPA  
 INFORMATION FOR SEQ ID NO: 52:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 36  
 TYPE: nucleic acid  
 STRANDEDNESS: single stranded  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA  
 HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 US-08-951-923-52

Query Match 0.7%; Score 15; DB 3; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 7.2e-02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

---

RESULT 19  
 US-08-724-586-3/c  
 ; Sequence 3, Application US/08724586  
 ; Patent No. 6066469  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Kruzel, Marian L.  
 ; APPLICANT: Kurecki, Tomasz  
 ; APPLICANT: Gollnick, Paul D.  
 ; APPLICANT: Doyle, Darrell J.

INFORMATION FOR SEQ ID NO: 51:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 31 base Pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: other nucleic acid  
 DESCRIPTION: /desc = "PCR primer"  
 US-08-942-423-51

TITLE OF INVENTION: Cloning, Expression, and Uses of Human Lactoferrin  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Jacobson, Price, Holman & Stern  
 STREET: 400 Seventh St. N.W.  
 CITY: Washington D.C.  
 COUNTRY: U.S.A.  
 ZIP: 20004  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US 08/724,586  
 FILING DATE: 30-SEPT-1996  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION NUMBER: US 08/238,445  
 APPLICATION NUMBER: US 08/238,445  
 FILING DATE: 05-MAY-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Player, William E.  
 REGISTRATION NUMBER: 31,409  
 TELECOMMUNICATION INFORMATION:  
 REFERENCE/DOCKET NUMBER: 10505/P58185C  
 TELEPHONE: (202) 638-6666  
 TELEFAX: (202) 393-5340  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 36 base pairs  
 STRANDEDNESS: single  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLogy: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 US-08-724-586-3

Query Match 0.7%; Score 15; DB 3; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1460 cctacggccgatcc 1474  
 ||||| ||||| |||||  
 Db 18 CCTACGGCCGATCC 4

RESULT 20  
 US-09-421-632-3/C  
 Sequence 3, Application US/09421632  
 ; Patent No. 6277817  
 GENERAL INFORMATION:  
 ; APPLICANT: Krueckl, Marian L.  
 ; APPLICANT: Kureckl, Tomasza  
 ; APPLICANT: Gollnick, Paul D.  
 ; APPLICANT: Doyle, Darrel J.  
 ; TITLE OF INVENTION: Cloning, Expression, and Uses of Human Lactoferrin  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Jacobson, Price, Holman & Stern  
 ; STREET: 400 Seventh St. N.W.  
 ; CITY: Washington D.C.  
 ; COUNTRY: U.S.A.  
 ; ZIP: 20004  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:



Db 24 GGCAGGGCAAGGGGT 38

RESULT 24  
US-09-461-697-78/C  
; Sequence 78, Application US/09461697  
; Patent No. 6277974  
; GENERAL INFORMATION:  
; APPLICANT: COGENT NEUROSCIENCE, Inc.  
; APPLICANT: Lo, Donald C.  
; APPLICANT: Barney, Shawn  
; APPLICANT: Thomas, Mary Beth  
; APPLICANT: Portbury, Stuart D.  
; APPLICANT: Puranam, Kasturi  
; APPLICANT: Katz, Lawrence C.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING,  
; TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING  
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING  
; FILE REFERENCE: 10001-005-999  
; CURRENT APPLICATION NUMBER: US/09/461,697  
; NUMBER OF SEQ ID NOS: 466  
; SOFTWARE: Fast-SEQ for Windows Version 4.0  
; SEQ ID NO 78  
; LENGTH: 105  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FILE REFERENCE: 10001-005-999  
; CURRENT FILING DATE: 1999-12-14

Query Match 0.7%; Score 15; DB 4; Length 105;  
Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 75 atggctctgaggga 89  
Db 75 ATGGCCTGAGGGGA 61

RESULT 25  
US-08-584-040-7661  
; Sequence 7661, Application US/08584040  
; Patent No. 6346398  
; GENERAL INFORMATION:  
; APPLICANT: Pavco, Pamela  
; APPLICANT: McSwiggen, James  
; APPLICANT: Stinchcomb, Dan T.  
; APPLICANT: Escobedo, Jaine  
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
; TREATMENT OF DISEASES OR  
; CONDITIONS RELATED TO LEVELS  
; TITLE OF INVENTION: GROWTH FACTOR  
; NUMBER OF SEQUENCES: 8502  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; SUITE: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066

COMPUTER READABLE FORM:  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/584,040  
FILING DATE: January 11, 1996  
CLASSIFICATION: 514  
PRIORITY APPLICATION DATA:

Query Match 0.7%; Score 14; DB 4; Length 17;  
Best Local Similarity 71.4%; Pred. No. 2.2e+02;  
Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1300 gacttgcctgc 1313  
Db 4 GACGUUGGCCUGGC 17

RESULT 26  
US-08-105-483-197/C  
; Sequence 197, Application US/08105483  
; Patent No. 549807  
; GENERAL INFORMATION:  
; APPLICANT: Paolelli, Enzo  
; TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE  
; TITLE OF INVENTION: STRAIN  
; NUMBER OF SEQUENCES: 462  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Curtis, Morris & Staffard  
; STREET: 530 Fifth Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/105,483  
; FILING DATE: 12-AUG-1993  
; CLASSIFICATION: 424  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 07/847,951  
; FILING DATE: 06-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Frommer, William S.  
; REGISTRATION NUMBER: 25,506  
; REFERENCE/DOCKET NUMBER: 454310-2400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 840-3333  
; TELEFAX: (212) 840-0712  
; INFORMATION FOR SEQ ID NO: 197:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-105-483-197

Query Match 0.7%; Score 14; DB 1; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 27  
 US-08-220-151-78/c  
 Sequence 78, Application US/08220151.  
 Patent No. 552980

GENERAL INFORMATION:  
 APPLICANT: Paolletti, Enzo  
 ATTORNEY/AGENT INFORMATION:  
 APPLICANT: Limbach, Keith J.

TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF CANINE HERPESVIRUS 9B, 9C AND 9D AND USES THEREFOR

NUMBER OF SEQUENCES: 91

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Curtis, Morris & Safford  
 STREET: 530 Fifth Avenue  
 CITY: New York  
 STATE: NY  
 ZIP: 10036

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/220,151  
 FILING DATE: 30-MAR-1994

CLASSIFICATION:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/220,151  
 FILING DATE: 30-MAR-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Frommer, William S.  
 REGISTRATION NUMBER: 25,506  
 REFERENCE/DOCKET NUMBER: 454310-2670  
 TELEPHONE: (212) 840-3333  
 TELEFAX: (212) 840-0712  
 INFORMATION FOR SEQ ID NO: 78:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 18 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA

US-08-413-118-78

RESULT 29  
 US-08-224-657-54/c  
 Sequence 54, Application US/08224657  
 Patent No. 5756102

GENERAL INFORMATION:  
 APPLICANT: Paoletti, Enzo  
 ATTORNEY/AGENT INFORMATION:  
 APPLICANT: Tartaglia, James

TITLE OF INVENTION: POXVIRUS - CANINE DISTEMPER VIRUS (CDV)  
 NUMBER OF SEQUENCES: 122

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Curtiss, Morris & Safford, P.C.  
 STREET: 530 Fifth Avenue  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10036

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/224,657  
 FILING DATE: 06-APR-1994  
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
 NAME: Frommer, William S.  
 REGISTRATION NUMBER: 25,506  
 REFERENCE/DOCKET NUMBER: 454310-2540  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 840-3333  
 TELEFAX: (212) 840-0712  
 TELEX: 425066 CURTMS

INFORMATION FOR SEQ ID NO: 78:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 18 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA

US-08-220-151-78

RESULT 28  
 US-08-413-118-78/c  
 Sequence 78, Application US/08413118  
 Patent No. 5688920

GENERAL INFORMATION:  
 APPLICANT: PAOLETTI, ENZO  
 ATTORNEY/AGENT INFORMATION:  
 APPLICANT: LIMBACH, KEITH J.  
 TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES OF CANINE HERPESVIRUS 9B, 9C, AND 9D AND USES THEREFOR  
 NUMBER OF SEQUENCES: 128

CORRESPONDENCE ADDRESS:

NAME: Frommer, William S.  
 REGISTRATION NUMBER: 25,506  
 REFERENCE/DOCKET NUMBER: 454310-2550  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 840-3333  
 TELEFAX: (212) 840-0712  
 TELEX: 425066 CORTMS  
 INFORMATION FOR SEQ ID NO: 54:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 18 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-08-224-657-54

RESULT 30  
 Query Match Score 0.7%; Best Local Similarity 100.0%; Pred. No. 2.2e+03; Mismatches 0; Indels 0; Gaps 0;  
 Sequence 197, Application US/08458101  
 Patent No. 5766599  
 GENERAL INFORMATION:  
 APPLICANT: Paoletti, Enzo  
 APPLICANT: Pertus, Marion E.  
 APPLICANT: Taylor, Jill  
 APPLICANT: Taragliis, James  
 APPLICANT: No. 576659ton, Elizabeth K.  
 APPLICANT: Riviere, Michel  
 APPLICANT: de Taisne, Charles  
 APPLICANT: Limbach, Keith J.  
 APPLICANT: Johnson, Gerard P.  
 APPLICANT: Pincus, Steven E.  
 APPLICANT: Cox, William I.  
 APPLICANT: Audonnet, Jean-Christophe Francis  
 APPLICANT: Gettig, Russell Robert  
 TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE  
 TITLE OF INVENTION: STRAIN

NUMBER OF SEQUENCES: 467  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Curtis, Morris & Safford  
 ADDRESSEE: C/O William S. Frommer  
 STREET: 530 Fifth Avenue  
 CITY: New York  
 STATE: NY  
 COUNTRY: USA  
 ZIP: 10036  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/709209  
 FILING DATE: 21-AUG-1996  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/105,483  
 FILING DATE: 12-AUG-1993  
 APPLICATION NUMBER: US 07/647,951  
 FILING DATE: 06-MAR-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Frommer, William S.  
 REGISTRATION NUMBER: 25,506  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 840-3333  
 TELEFAX: (212) 840-0712  
 INFORMATION FOR SEQ ID NO: 197:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 18 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-224-657-54

RESULT 31  
 Query Match Score 0.7%; Best Local Similarity 100.0%; Pred. No. 2.2e+03; Mismatches 0; Indels 0; Gaps 0;  
 Sequence 197, Application US/08458101  
 Patent No. 5766599  
 GENERAL INFORMATION:  
 APPLICANT: Paoletti, Enzo  
 APPLICANT: Pertus, Marion E.  
 APPLICANT: Taylor, Jill  
 APPLICANT: Taragliis, James  
 APPLICANT: No. 576659ton, Elizabeth K.  
 APPLICANT: Riviere, Michel  
 APPLICANT: de Taisne, Charles  
 APPLICANT: Limbach, Keith J.  
 APPLICANT: Johnson, Gerard P.  
 APPLICANT: Pincus, Steven E.  
 APPLICANT: Cox, William I.  
 APPLICANT: Audonnet, Jean-Christophe Francis  
 APPLICANT: Gettig, Russell Robert  
 TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE  
 TITLE OF INVENTION: STRAIN

NUMBER OF SEQUENCES: 467  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Curtis, Morris & Safford  
 ADDRESSEE: C/O William S. Frommer  
 STREET: 530 Fifth Avenue  
 CITY: New York  
 STATE: NY  
 COUNTRY: USA  
 ZIP: 10036  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/458,101  
 FILING DATE: 01-JUN-1995  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Frommer, William S.  
 REGISTRATION NUMBER: 25,506  
 REFERENCE/DOCKET NUMBER: 454310-2740  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 840-3333  
 TELEFAX: (212) 840-0712  
 INFORMATION FOR SEQ ID NO: 197:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 18 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-458-101-197

RESULT 32  
 Query Match Score 0.7%; Best Local Similarity 100.0%; Pred. No. 2.2e+03; Mismatches 0; Indels 0; Gaps 0;  
 Sequence 197, Application US/08458101  
 Patent No. 5766599  
 GENERAL INFORMATION:  
 APPLICANT: Paoletti, Enzo  
 APPLICANT: Pertus, Marion E.  
 APPLICANT: Taylor, Jill  
 APPLICANT: Taragliis, James  
 APPLICANT: No. 576659ton, Elizabeth K.  
 APPLICANT: Riviere, Michel  
 APPLICANT: de Taisne, Charles  
 APPLICANT: Limbach, Keith J.  
 APPLICANT: Johnson, Gerard P.  
 APPLICANT: Pincus, Steven E.  
 APPLICANT: Cox, William I.  
 APPLICANT: Audonnet, Jean-Christophe Francis  
 APPLICANT: Gettig, Russell Robert  
 TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE  
 TITLE OF INVENTION: STRAIN

NUMBER OF SEQUENCES: 467  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Curtis, Morris & Safford  
 ADDRESSEE: C/O William S. Frommer  
 STREET: 530 Fifth Avenue  
 CITY: New York  
 STATE: NY  
 COUNTRY: USA  
 ZIP: 10036  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/458,101  
 FILING DATE: 01-JUN-1995  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Frommer, William S.  
 REGISTRATION NUMBER: 25,506  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 840-3333  
 TELEFAX: (212) 840-0712  
 INFORMATION FOR SEQ ID NO: 197:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 18 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-458-101-197

US-08-184-009-52/C  
 Sequence 52, Application US/08184009  
 Patent No. 5333975  
 GENERAL INFORMATION:  
 APPLICANT: Paoletti, Enzo  
 APPLICANT: Tartaglia, James  
 APPLICANT: Cox, William I.  
 TITLE OF INVENTION: RECOMBINANT VIRUS IMMUNOTHERAPY  
 NUMBER OF SEQUENCES: 217  
 CORRESPONDENCE ADDRESS:  
 STREET: 530 Fifth Avenue  
 CITY: New York  
 STATE: NY  
 COUNTRY: USA  
 ZIP: 10036

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/184.009  
 FILING DATE: 19-JAN-1994  
 CLASIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
 NAME: Frommer, William S.  
 REGISTRATION NUMBER: 25,506  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 840-3333  
 TELEFAX: (212) 840-0712

INFORMATION FOR SEQ ID NO: 52:  
 LENGTH: 18 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 STRANDEDNESS: linear  
 MOLECULE TYPE: cDNA

US-08-184-009-52

Query Match 0.7%; Score 14; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 gatgaaaggatgta 69  
 Db 14 GATGAGGACGTGA 1

RESULT 33  
 US-08-173-489C-11  
 Sequence 11, Application US/08173489C  
 Patent No. 5881244

GENERAL INFORMATION:  
 APPLICANT: WANG, C. -G.  
 APPLICANT: HEPPURN, A. G.  
 TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA  
 TITLE OF INVENTION: TRIPLE-STRAND FORMATION.  
 NUMBER OF SEQUENCES: 365

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,  
 STREET: 510 EAST 73RD STREET,  
 CITY: NEW YORK  
 STATE: NEW YORK  
 COUNTRY: USA  
 ZIP: 10021.

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.44Mb storage  
 COMPUTER: IBM PC/XT/AT  
 OPERATING SYSTEM: MS-DOS version 6.2

SOFTWARE: Wordperfect version 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/173,489C  
 FILING DATE: 22 DEC 1993  
 CLASSIFICATION: 435  
 PRIOR APPLICATION NUMBER: US 07/968,436  
 APPLICATION NUMBER: 29 OCT 1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Handelman, Joseph H.  
 REGISTRATION NUMBER: 26,179  
 REFERENCE/DOCKET NUMBER: US9518-6  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (attorney) (212) 708-1880  
 TELEFAX: (attorney) (212) 246-8959  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 18 base pairs  
 TYPE: Nucleic Acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: Genomic DNA  
 DESCRIPTION: c-myc gene (Accession # X00364,  
 DESCRIPTION: K01908, V00501) nucleotides 6663 to 6680  
 HYPOTHETICAL: No  
 ANTI-SENSE: No  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 PUBLICATION INFORMATION:  
 AUTHORS: Gazin, C., Dupont, S., de Dinechin, D.,  
 AUTHORS: Hampe, A., Masson, J M., Martin, P., Steehelin,  
 AUTHORS: D., Galibert, F.  
 TITLE: Nucleotide sequence of the  
 human c-myc locus: provocative open reading  
 frame within the first exon.  
 JOURNAL: EMBO Journal  
 VOLUME: 3  
 PAGES: 383-387  
 DATE: 1984  
 AUTHORS: Colby, W W., Chen, E Y., Smith, D H.,  
 AUTHORS: Levinson, A. D.  
 TITLE: Identification and nucleotide  
 sequence of a human locus homologous to the v-  
 myc oncogene of avian myelocytomatosis virus  
 TITLE: mc29  
 JOURNAL: Nature  
 VOLUME: 301  
 PAGES: 722-725  
 DATE: 1983  
 AUTHORS: Saito, H., Hayday, A C., Witman, K G.,  
 AUTHORS: Hayward, W S., Tongeawa, S.,  
 TITLE: Activation of the c-myc gene  
 by translocation: a model for translational  
 control  
 JOURNAL: Proceedings of the National Academy of  
 Sciences, USA  
 VOLUME: 80  
 PAGES: 7476-7480  
 DATE: 1983  
 AUTHORS: Gazin, C., Rigollet, M., Briand, J P., Van  
 AUTHORS: Regemortel, M H V., Galibert, F.  
 TITLE: Immunochemical detection of the human c-myc exon 1  
 TITLE: proteins related to the human c-myc exon 1  
 JOURNAL: EMBO Journal  
 VOLUME: 5  
 PAGES: 2241-2250  
 DATE: 1986  
 PAGES: RELEVANT RESIDUES IN SEQ ID NO: 11 :FROM 1 TO 18  
 US-08-173-489C-11

Query Match 0.7%; Score 14; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 gatgaaaggatgta 69  
 Db 14 GATGAGGACGTGA 1

RESULT 33  
 US-08-173-489C-11  
 Sequence 11, Application US/08173489C  
 Patent No. 5881244

GENERAL INFORMATION:  
 APPLICANT: WANG, C. -G.  
 APPLICANT: HEPPURN, A. G.  
 TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA  
 TITLE OF INVENTION: TRIPLE-STRAND FORMATION.  
 NUMBER OF SEQUENCES: 365

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,  
 STREET: 510 EAST 73RD STREET,  
 CITY: NEW YORK  
 STATE: NEW YORK  
 COUNTRY: USA  
 ZIP: 10021.

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.44Mb storage  
 COMPUTER: IBM PC/XT/AT  
 OPERATING SYSTEM: MS-DOS version 6.2

Query Match 0.7%; Score 14; DB 2; Length 18;  
 Best local similarity 100.0%; Pred. No. 2.e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 11 gaagatgaggaga 24  
 Db 3 GAAGATGAGGAAGA 16

RESULT 34  
 US-08-417-210A-52/c  
 Sequence 52, Application US/08417210A  
 Patent No. 5853542  
 GENERAL INFORMATION:  
 APPLICANT: PAOLETTI, ENZO  
 APPLICANT: TARPIAGLIA, JAMES  
 APPLICANT: COX, WILLIAM I.  
 TITLE OF INVENTION: IMMUNODEFICIENCY RECOMBINANT POXVIRUS  
 NUMBER OF SEQUENCES: 148  
 CURRENT APPLICATION DATA:  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.  
 STREET: 530 FIFTH AVENUE  
 CITY: NEW YORK  
 STATE: NEW YORK  
 COUNTRY: USA  
 ZIP: 10036  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Versión #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/417,210A  
 FILING DATE: 05-APR-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KOWALSKI, THOMAS J.  
 REGISTRATION NUMBER: 32,147  
 REFERENCE/DOCKET NUMBER: 454310-2690  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-840-3333  
 INFORMATION FOR SEQ ID NO: 52:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 18 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-08-417-210A-52

Query Match 0.7%; Score 14; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 gatgaagacatga 69  
 Db 14 GATGAAGACATGA 1

RESULT 35  
 US-08-585-684B-273/c  
 Sequence 273, Application US/085856843  
 Patent No. 5877021  
 GENERAL INFORMATION:  
 APPLICANT: Stinchcomb, Daniel T.  
 APPLICANT: Jarvis, Thale  
 APPLICANT: McSwiggen, James  
 TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
 INDUCTION OF GRAFT TOLERANCE  
 TITLE OF INVENTION: INDUCTION OF IMMUNE RESPONSES  
 NUMBER OF SEQUENCES: 2751  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street

STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: FASTSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/585,684B  
 FILING DATE: January 16, 1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/000,951  
 FILING DATE: July 7, 1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Warburg, Richard  
 REGISTRATION NUMBER: 32,327  
 REFERENCE/DOCKET NUMBER: 218/078  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 2737:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 18 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-585-684B-2737

Query Match 0.7%; Score 14; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1155 cagcaagcagccat 1168  
 Db 15 CAGCAAGCAGCCAT 2  
 Search completed: May 17, 2002, 18:18:30  
 Job time: 6691 sec





Result No.	Score	Query %	Match Length	DB ID	Description
c 1	18	0.9	20	2 US-08-910-629A-31	Sequence 31, Appl
c 2	18	0.9	20	2 US-09-620A-42	Sequence 42, Appl
c 3	18	0.9	20	3 US-09-269-668-7	Sequence 7, Appl
c 4	18	0.9	20	3 US-09-287-796-31	Sequence 31, Appl
c 5	18	0.9	20	3 US-09-287-796-42	Sequence 42, Appl
c 6	18	0.9	20	4 US-09-130-616-31	Sequence 31, Appl
c 7	18	0.9	20	4 US-09-130-616-42	Sequence 42, Appl
c 8	17	0.8	20	2 US-08-750-876-2	Sequence 2, Appl
c 9	17	0.8	20	4 US-09-190-692-71	Sequence 71, Appl
c 10	17	0.8	23	1 US-08-222-616-2	Sequence 2, Appl
c 11	17	0.8	23	5 PCT-US95-042282	Sequence 2, Appl
c 12	16	0.8	24	2 US-08-859-998-598	Sequence 598, Appl
c 13	16	0.8	24	4 US-09-225-928-598	Sequence 598, Appl
c 14	15	0.7	18	3 US-08-951-923-51	Sequence 51, Appl
c 15	15	0.7	18	4 US-08-564-040-6218	Sequence 6218, Appl
c 16	15	0.7	19	1 US-08-400-580A-11	Sequence 11, Appl
c 17	15	0.7	31	2 US-08-942-423-51	Sequence 51, Appl
c 18	15	0.7	36	3 US-08-951-923-52	Sequence 52, Appl
c 19	15	0.7	36	3 US-08-724-586-3	Sequence 3, Appl
c 20	15	0.7	36	4 US-09-421-632-3	Sequence 3, Appl
c 21	15	0.7	45	2 US-08-039-198B-3	Sequence 47, Appl
c 22	15	0.7	72	2 US-08-07-231A-47	Sequence 19, Appl
c 23	15	0.7	104	3 US-09-058-399A-19	Sequence 78, Appl
c 24	15	0.7	105	4 US-09-161-697-78	Sequence 7661, Appl
c 25	14	0.7	17	4 US-08-584-040-7661	Sequence 197, Appl
c 26	14	0.7	18	1 US-08-105-483-197	Sequence 2/37, Appl
c 27	14	0.7	18	1 US-08-220-151-78	Sequence 52, Appl

## SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## ALIGNMENTS

RESULT	1	US-08-910-629A-31/c	Sequence 31, Application US/08910629A
		/ Patent No. 5,877,309	/ GENERAL INFORMATION:
		/ APPLICANT: Robert A. McKay	/ APPLICANT: Nicholas M. Dean
		/ APPLICANT: Brett Monia	/ TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE
		/ NUMBER OF SEQUENCES: 86	/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE MODULATION OF JNK
		/ CORRESPONDENCE ADDRESS:	/ TITLE OF INVENTION: PROTEINS
		/ ADDRESSE: Law Offices of Jane Massey Licata	/ COUNTRY: USA
		/ STREET: 66 East Main Street	/ CITY: Marlton
		/ STATE: NJ	/ ZIP: 08053
		/ COMPUTER READABLE FORM:	/ SOFTWARE: WORDPERFECT 6.1
		/ MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB	/ OPERATING SYSTEM: WINDOWS 95
		/ MEDIUM TYPE: STORAGE	/ COMPUTER: PENTIUM

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/910,629A  
 FILING DATE: August 13, 1997  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:



```

; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0215
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; US-08-910-629A-31

; ANTI-SENSE: NO
; US-08-910-629A-42

Query Match 0.9%; Score 18; DB 2; Length 20;
Best Local Similarity 100.0%; Prod. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1300 gacttggctggcccg 1317
Db 20 GACTTGGCTGGCCCG 3

RESULT 3
US-09-209-668-7/c
Sequence 7, Application US/09209668A
; Patent No. 6114517
; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR
; FILE REFERENCE: ISPH-0336
; CURRENT APPLICATION NUMBER: US/09/209,668A
; CURRENT FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-09-209-668-7

Query Match 0.9%; Score 18; DB 3; Length 20;
Best Local Similarity 100.0%; Prod. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1300 gacttggctggcccg 1317
Db 20 GACTTGGCTGGCCCG 3

RESULT 4
US-09-287-796-31/c
Sequence 31, Application US/09287796A
; Patent No. 6133246
; GENERAL INFORMATION:
; APPLICANT: McKay, Robert A.
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Nero, Pam
; APPLICANT: Gaarde, William A.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE COMPOSITIONS AND METHODS
; FILE REFERENCE: ISPH-0350
; CURRENT APPLICATION NUMBER: US/09/287,796A
; CURRENT FILING DATE: 1999-04-07
; EARLIER APPLICATION NUMBER: 09/130,616
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 08/910,629
; EARLIER FILING DATE: 1997-08-03
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 31
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-287-796-31

; ANTI-SENSE: USA
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
; COMPUTER: PENTIUM
; COMPUTER: PENTIUM
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,629A
; FILING DATE: August 13, 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; TELECOMMUNICATION INFORMATION:
; REFERENCE/DOCKET NUMBER: ISPH-0215
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear

```



308-10-#6

MAY 18 14:43:30 2002

us-10-007-010-3.rng

Page 11

file

KW polymerase chain reaction; ss.  
 XX OS Synthetic.  
 XX PN WO9514772-A1.  
 XX PD 01-JUN-1995.  
 XX PF 11-NOV-1994; 94WO-JP01916.  
 XX PR 12-NOV-1993; 93JP-0355504.  
 XX PA (MATS//) MATSUBARA K.  
 PA (OKUB//) OKUBO K.  
 PI Matsubara K; Okubo K;  
 XX DR WPI; 1995-206931/27.  
 PS Example 7; Fig 8; 224pp; Japanese.

PT Identifying gene signatures in 3'-directed human cDNA library - e.g.  
 PT for diagnosis of abnormal cell function, by preparing cDNA that  
 PT reflects relative abundance of corresp. mRNA in specific human  
 PT tissues

XX PS Sequence 20 BP; 2 A; 6 C; 4 G; 8 T; 0 other;

Query Match Score 1.0%; Score 20; DB 16; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1673 aacagaggccatgtatggaa 1692  
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 Db 20 AACAGGCCGCGATAGGA 1

Query Match Score 0.9%; Score 19; DB 22; Length 51;  
 Best Local Similarity 100.0%; Pred. No. 61;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1232 actacatccaccgacact 1250  
 ||||| ||||| ||||| ||||| |||||  
 Db 25 ACTACATCCACCGAAGACCT 7

RESULT #23  
 AA133025 standard; DNA; 51 BP.  
 DE Human SNP oligonucleotide #6233.  
 XX KW Immunosuppressive; immunostimulatory; antiinflammatory; cytotoxic;  
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;  
 KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;  
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease; ss.  
 XX OS Homo sapiens.  
 XX PN WO200147944-A2.  
 XX PN 05-JUL-2001.

